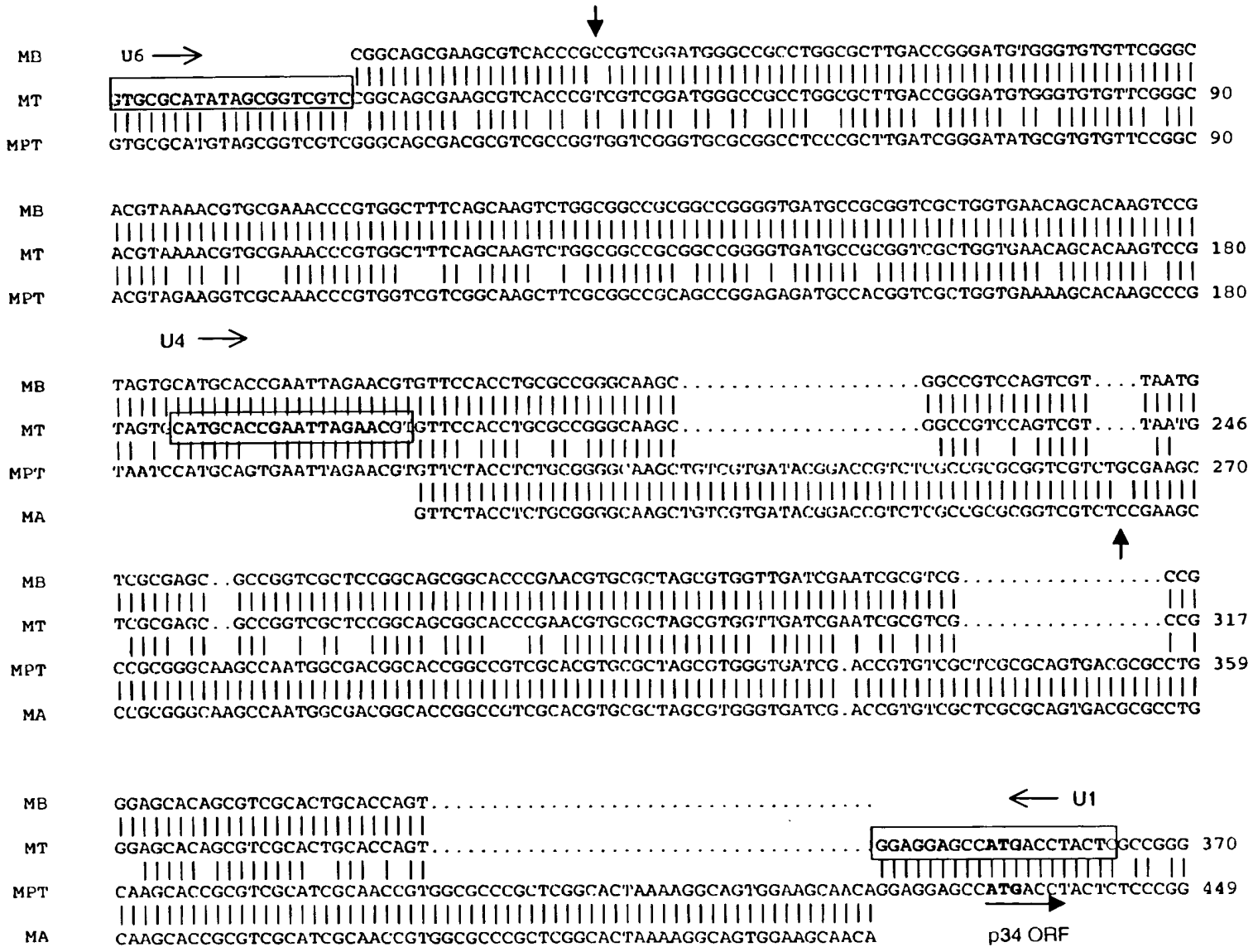
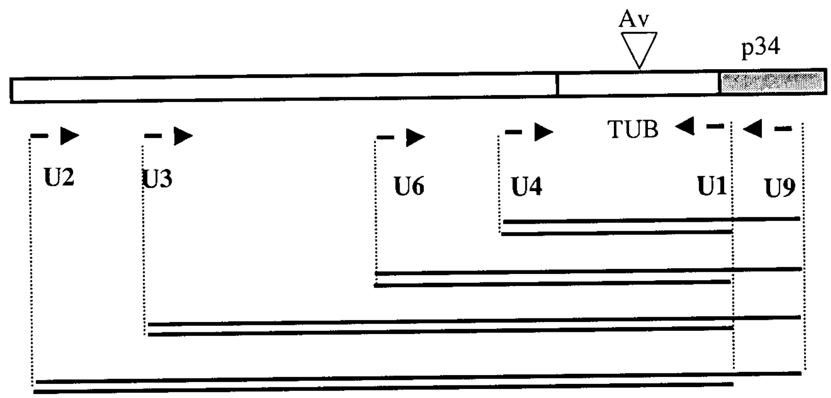


Figure 1.

Figure 2. Amplifications of us-p34 regions with primers U1, U2, U3, U4, U6 and U9.



Open Reading Frame of p34

79 bp deletion of the us-p34 region of tuberculous mycobacteria (TUB)

Primer

Figure 3. New us-p34 sequences (5' to 3')

Primers used to obtain the sequence (either U2-U1 ; U3-U1 ; U4-U1 ; U2-U9 ; U3-U9 or U4-U9) and the amplicon size are as indicated. Sequence variations (point mutations) found in the same species (for instances *M. ulcerans*) are also indicated when known.

M. intracellulare U4-U1 Length: 216 (SEQ ID NO 57)

```
  1 GTTCTACCTG TGCTGAGCAA GCTCCGGTGA TACCGACCGT CTCGCCGGAG
 51 GGCCGCCGGG GGCCTCGCCG CCCAAGACAG TGGCGGCGCC ACCGGTTCCC
101 GCACGTGCGC TAGCGTGGGT GATCGACCGC GTCGCAATGC GGTGACGCGC
151 CTGCAAGCAC AGCGTCGCAT CGCCACCGCG GCGCCCGCTC GGCACTTAAA
201 GGCACTGGTA GCAACA
```

M. avium U2-U9 Length: 881 (SEQ ID NO 58)

Underlined, the mutated nucleotide which allows to differentiate *M. avium* from *M. paratuberculosis*.

```
  1 TCGTAGCTGG CTTCCTCGTC GGTCCACAGC GCCCGCATCG CTTCCAGGTA
 51 TTCGCGCAGC ATGGTGCGGC GCCGGCCCGC CGGCACGCCG TGGTCGGCGA
101 GTTCGTCGGT GTTCCAGCCG AACCCGACGC CGAGGCTGAC CCGGCCGCCG
151 GACAGATGGT CAAGGGTGGC AATACTTTTC GCCAGCGTGA TCGGGTCGTG
201 TTCGACCGGC AGGGCCACCG CGGTGGACAG CCGCACCCGC GAGGTGACGG
251 CACAGGCCGC GCCCAGACTG ACCCACGGGT CCAGGGTGCG CATGTAGCGG
301 TCGTCGGGCA GCGACGCGTC GCCGGTGGTC GGGTGCGCGG CCTCCCGCTT
351 GATCGGGATA TGCGTGTGTT CCGGCACGTA GAAGGTCGCA AACCCGTGGT
401 CGTCGGCAAG CTTCGCGGCC GCAGCCGGAG AGATGCCACG GTCGCTGGTG
451 AAAAGCACAA GCCCGTAATC CATGCAGTGA ATTAGAACGT GTTCTACCTC
501 TGCGGGGCAA GCTGTCGTGA TACGGACCGT CTCGCCGCGC GGTCGTCTCC
551 GAAGCCCGCG GGCAAGCCAA TGGCGACGGC ACCGGCCGTC GCACGTGCGC
601 TAGCGTGGGT GATCGACCGT GTCGCTCGCG CAGTGACGCG CCTGCAAGCA
651 CCGCGTCGCA TCGCAACCGT GGCGCCCGCT CGGCACTAAA AGGCAGTGGA
701 AGCAACAGGA GGAGCCATGA CCTACTCTCC CGGCAGCCCC GGATATCCAC
751 CGGCGCAGTC TGGCGGCACC TATGCAGGCG CCACACCATC TTTCGCCAAA
801 GACGACGACG GCAAGAGCAA ACTCCCGCTC TACCTCAACA TCGCCGTGGT
851 CGCCCTGGGT TTCGCGGCCT ACCTGCTGAA T
```

M. gastri U3-U1 Length: 642 (SEQ ID NO 59)

1 GTGCGCCGGC GCCCCGGCGG CACGCCATGG TCGGCGAGTT CGTGCGCCCG
51 GCGGCACGCC ATGGTCGGCG AGTTCGTCGG TGTTCCAGCC GAATCCGACG

Figure 3-continued

101 CCGACGCTGA CCCGGCCCCC GGATAGTGGT CCAGCGTGGC AATGCTTTTG
151 GCCAGCGTGA TCGGGTCATG CTCCACCGCA GCGCAACCGC GGTTGACAGC
201 CTGACTCGGG AGGTGACCGC TGAAGCCGCA CCCAAGCTCA CCCACGGGTC
251 CAGGGTGCGC ATATAGCGGT CGTCCGGCAG CGACGCGTCA CCCGTCGTGG
301 GATGGGCGGC TTCCCGTTTG ACCGGGATAT GCGTGTGTTC GGGCACGTAG
351 AGAGTGCGAA AGCCATGGTC GTCGGCCAGT TTCGCGGCTG CCGCCGGGGA
401 GATCCCACGG TCGCTGGTGA AAAGGACAAG CCCGTAATCC ATGAACAGAA
451 TTAGAACGTG TTCTACCTCC GCCGGGCAAG CGGCTCATCT GCCGATCGGC
501 AGCGGTGCCG GGGCCGGTAT CGCGGGCGGC AAGGTCGCCA CGGCGTGAGT
551 ACCCGGCCGT GCGCTAGCGT GGGTCATCGA ATTGTGTCGC AGGGAGCAAT
601 CGTCGCATTG CAGCAGGCGT AGCGACGGCA CCGGAGGTAA CA

M. gordonae U3-U9 Length: 745 (SEQ ID NO 60)

1 GTGCGACGAC GGCCGGCCAG CACGTTATGG TCGGCGAGCT CGTCGGTGTT
51 CCAGCCGAAC CCGACGCCGA GGCTAACTCG CCCGCCGGAC AGGTGATCCA
101 GCGTGGCGAT GCTTTTCGCC AAGGTGATCG GGTCATGCTC GACCGGCAAC
151 GCGACTGCCG TCGACAGCCG CACCCGCGAC GTCACAGCAC ACGCCGCGCC
201 CAGGCTCACC CAGGGATCCA GGGTGCGCAT ATAACGGTCG TCGGGCAGCG
251 TCTCGTCTCC GGTGGTGGGA TGAGCCGCCT CGCGTTTGAT CGGGATATGC
301 GTGTGTTCGG GTACGTAGAA GGTGTGAAAA CCATGTGTGT CGGCAAGTTT
351 CGCTGCTGCC GCAGGGGAAA TACCGCGATC GCTGGTGAAC AGAACGAGGC
401 TGTAGTCCAT GCCCCAATTT AGAACGTGTT CTACTTTTGG CCGCAGCCGA
451 CCCCCTGCGG CGACGGGCAC TAGTTGTCAG AGGTGCGCTA GCGTGGTTGA
501 TCGAATGCGT CGCAGGCCGT ACCGCGTCGT GCCGAAGCAG AGGGGCCGTG
551 ACGGCACCGG AAGCAACAGG AGGACTTATG ACCTACCCGC CCGGTAGTCC
601 CGGATATCCA TCCGCCCAGC AGTCGGCCGG CAACTACGGC AGCTCCGCTC
651 CCGCCGCCGG CCAGTCCGAG CCGGGTGAAA GCAAGCTGGG ACTGTACCTG
701 GCCATCGCGG TGGCGGCCCT GGGCCTACTG GCGTACCTCT TCAGC

M. kansasii U3-U9 Length: 785 (SEQ ID NO 61)

1 GTGCGCCGGC GCGCCGGCGG CACGCCATGG TCAGCGAGTT CGTCGGTGTT
51 CCAGCCGAAT CCGACGCCGA CGCTGACCCG CCCCCCGGAT AGGTGGTCCA

```
101  GCGTGGCAAT GCTTTTGGCC AGCGTGATCG GGTCATGCTC GACCGGCAAC
151  GCAACCGCTG TTGACAGTCG GACCCGGAAG GTGACCGCTG AAGCCGCGCC
201  CAAACTCACC CACGGGTCCA GCGTGCGCAT ATAGCGGTCG TCCGGCAGCG
251  ACGCGTCACC CGTCGTGGGA TGGCGGCCTC CCGTTTGACC GGGATGTGCG
301  TGTGTTCGGG CACGTAGAAA GTGCGAAAGC CATGGTCGTC GGCCAGTTTC
351  GCGGCTGCCG CGGGAGAAAT GCCACGGTCG CTGGTGAAAA GGACAAGCCC
```

Figure 3-continued

```
401  GTAATCCATG AACAGAATTA GAACGTGTTC TACCTCAGCC GGGCAAGCGG
451  CTCATCCGCC GATCGTCGGC AGTGGTGACG GGGCCGGTAT CACGGGGGCA
501  AGGTCGCCAC GGCGCGAGTA CCAGGCCGTG CGCTAGCGTG GGTCATCGAA
551  TCGTGTCGCA GGGAGCAATC GTCGCATTGC AGCAGGCGTA GCGACGGCAC
601  TGGAGGTAAC AGGAGGAGCC ATGACCTACT CACCAGGTAG TCCCGGATAT
651  CCGCCCGCGC AATCGGCCGG CTCCTACGGA GCCGCCACAC CGTCTTTCGC
701  CAAGGCCGAC GACGGTGTCA GCAAGCTTCC GATGTACCTG AGCATGGCGG
751  TTGCCGCGCT CGGGCTGCTG GCGTATCTGG CCAGC
```

M. malmoense U2-U1 Length: 741 (SEQ ID NO 62)

```
  1  TCGTAGGCCG CTTCCTCCTG GGTCCACAGC GCCCGCATTG CCTCGATGTA
 51  TTCACGCAGC ATGGTGCGAC GGCGCCCGGC CGGCACGCCG TGGTCGGCGA
101  GCTCGTCGGT GTTCCAGCCA AACCCAACGC CGAGGCTGAC CCGGCCGCCG
151  GACAGGTGGT CCAAGGTGGC AATACTTTTC GCCAGCGTGA TCGGGTCGTG
201  CTCGACGGGC AGCGCCACCG CGGTAGACAG CCGCACCCGC GACGTCACGG
251  CGCACGCCGC GCCCAGGCTC ACCCACGGGT CTAGCGTGCG CATATAGCGG
301  TCGTCCGGCA AGCGACGCGC CACCCGTCGT CGGATGGGCC GCCTCGCGCT
351  TGACCGGGAT ATGGGTGTGT TCCGGCACGT AGAACGTCTG GAAGCCGTGG
401  TCGTCGGCAA GTTTGGCGGC TGCCGCCGGG GAGATGCCGC GGTCGCTGGT
451  GAAAAGTACA AGCCCGTAAT CCATGGACAG AATTAGAACG TGTTCTACCG
501  GCGGTGGGCA AGCCGCTGCG CCGCCGAGGA TCTCGACTCG GACCCACAAC
551  ACTGGTCGGC GCCGGGCGCG CCGACAGGTC GGTCGGCCCG GCACGGGCGG
601  CCGAACGTGC GCTAGCGTGG GTGATCGATC GCGTCGCAAC GCAAGATCTC
701  ATGCGGCGTC GCTGAGGGTC TTGAAGGCAC TGGAAGCAAT A
```

M. simiae U2-U1 Length: 748 (SEQ ID NO 63)

```
  1  TCGTATTGGG CTTCTTCCTG CGTCCACAGC GCCCGCATGG CTTCCAGGTA
 51  CTCGCGCAGC ATGGTCCGCC GGCGCGCCGG CGGCACGTTG TGGTCGGCCA
```

```
101  GTTCGTCGGT GTTCCAACCG AACCCGACGC CCACACTGAC CCGTCCGCCG
151  GACAGATGGT CCAGGGTGGC GATGCTTTTC GCCAGCGTGA TCGGGTCGTG
201  CTCGACGGGC AGCGCGACCG CGGTGGACAG TCGCACCCGC GAGGTGACCG
251  CGCACGCCGC GCCCAGACTG ACCCACGGGT CCAGCGTGCG CATGTAGCGG
301  TCGTCGGGCA GCGATTCGTC GCCCGTCGTG GGATGGGCCG CCTCGCGCTT
351  GATCGGGATG TGAGTGTGTT CTGGCACGTA GAACGTTGTG AAGCCATGGT
401  CGTCGGCGAG TTTGGCCGCG GCCGCCGGGG CGATGCCCCG ATCACTGGTG
451  AAAAGCACGA GCCCGTAATC CATGCACAGA ATTAGAACGT GTTCTACCTC
501  TGTGGAGCAA GCGGCCCCCG CTACGTCGAC CCGCAGACGG GCCGCTGAGA
```

Figure 3-continued

```
551  CGATCGCTCC TGGTCGCGCC TAGGGGCCGG TCGCTCCCGC GCACCCGCTC
601  GAACGTGCGC TAGCGTGGTT GATCGGTCGC GCGTAACGCA AACGCGGGCA
701  AGCAGTGACG TCGCGCCCGA CGAGGTCTTG AAGGCACTGG AAGCAACA
```

M. szulgai U3-U9 Length: 712 (SEQ ID NO 64)

```
  1  GTGCGGCGGC GCCCGGCCGG GACGCCGTGA TCAGCGAGCT CGTCGGTATT
 51  CCAGCCGAAG CCGACGCCGA GGCTGACCCG GCTGCCGGAC AGATGATCCA
101  GCGTGGCAAT GCTTTTGGCC AGCGTGATCG GATCATGCTC GACCGGCAGC
151  GCCACCGCGG TGGACAACCG GACCCGAGAC GTCACCGCGG CCGCAGCACC
201  CAAACTCACC CACGGGTCCA GCGTGCGCAT GTAGCGGTCA TCGGGCAGCG
251  ACGCGTCACT CGTAGTGGGA TGGGCAGCCT CCCGCTTGAT CGGGATGTGG
301  GTGTGTTCAG GCACGTAGAA CGTCTGAAAA CCGTGGTCGT CGGCCAGCTT
351  TGCGGCCGCC GCCGGGGCAA TGCCGCGATC GCTGGTGAAA AGTACAAGCC
401  CGTAATCCAT GCACCGAATT AGAACGTGTT CTACCTGCGA TGAGCAAGCG
451  GCCCGGTCGG CCGACGAGCA GGTCGGCCCG GCGCGACCAG CAGAACGTGC
501  GCTAGCGTGG TTGATCGAGT CGCGCACCGG AAAGCAACCG GAAGTAATCA
551  GGAGGAGCCA TGACCTACTC GACCGGCAGC CCCGGATATC CGCCTGCGCA
601  GCAGCCCGGG GGGTCGTACG GCGGCGCCAC TCCTGGTGAC GCTCAGAGCA
651  AGCTTCCGCT GTACCTCAGC ATGGCGGTGG CCGCCCTCGG CCTGGCCGCG
701  TATCTCGCCA GC
```

M. tuberculosis U2-U9 Length: 802 (SEQ ID NO 65)

```
  1  TCATAGCAGG CCTCCTCTTG GGTCCACAAC GCCCGCATCG CCTCGAGGTA
 51  TTCGCGCAGC ATGGTGCGGC GGCGTCCGGG TGGCACACCA TGATCGACGA
101  GCTCGTCGGT GTTCCAGCCG AACCCGACCC CGACGCTGAC CCGGCCGTGC
151  GACAAATGAT CCAGCGTCGC AATGCTTTTC GCCAGCGTGA TCGGATCATG
201  CTCGACCGGC AGCGCCACCG CGGTGGCAAG CCGGATCCGC GACGTCACCG
```

```
251  CCGATGCTGC TCCCAGGCTC ACCCACGGGT CCAACGTGCG CATATAGCGG
301  TCGTCCGGCA GCGAAGCGTC ACCCGTCGTC GGATGGGCCG CCTGGCGCTT
351  GACCGGGATG TGGGTGTGTT CGGGCACGTA AAACGTGCGA AACCCGTGGC
401  TTTCAGCAAG TCTGGCGGCC GCGGCCGGGG TGATGCCGCG GTCGCTGGTG
451  AACAGCACAA GTCCGTAGTG CATGCACCGA ATTAGAACGT GTTCCACCTG
501  CGCCGGGCAA GCGGCCGTCC AGTCGTTAAT GTCGCGAGCG CCGGTCGCTC
551  CGGCAGCGGC ACCCGAACGT GCGCTAGCGT GGTTGATCGA ATCGCGTCGC
601  CGGGAGCACA GCGTCGCACT GCACCAGTGG AGGAGCCATG ACCTACTCGC
651  CGGGTAACCC CGGATACCCG CAAGCGCAGC CCGCAGGCTC CTACGGAGGC
701  GTCACACCCT CGTTCGCCCA CGCCGATGAG GGTGCGAGCA AGCTACCGAT
751  GTACCTGAAC ATCGCGGTGG CAGTGCTCGG CCTGGCTGCG TACTTCGCCA
801  GC
```

Figure 3-continued

M. bovis U2-U1 Length: 628 (SEQ ID NO 66)

In this sequence, there is a mutation (as underlined) compared with the sequence of *M. tuberculosis*.

```
  1  TCATAGCAGG CCTCCTCTTG GGTCCACAAC GCCCGCATCG CCTCGAGGTA
 51  TTCGCGCAGC ATGGTGCGGC GGCGTCCGGG TGGCACACCA TGATCGACGA
101  GCTCGTCGGT GTTCCAGCCG AACCCGACCC CGACGCTGAC CCGGCCGTGC
151  GACAAATGAT CCAGCGTCGC AATGCTTTTC GCCAGCGTGA TCGGATCATG
201  CTCGACCGGC AGCGCCACCG CGGTGGCAAG CCGGATCCGC GACGTCACCG
251  CCGATGCTGC TCCCAGGCTC ACCCACGGGT CCAACGTGCG CATATAGCGG
301  TCGTCCGGCA GCGAAGCGTC ACCCGCCGTC GGATGGGCCG CCTGGCGCTT
351  GACCGGGATG TGGGTGTGTT CGGGCACGTA AAACGTGCGA AACCCGTGGC
401  TTTCAGCAAG TCTGGCGGCC GCGGCCGGGG TGATGCCGCG GTCGCTGGTG
451  AACAGCACAA GTCCGTAGTG CATGCACCGA ATTAGAACGT GTTCCACCTG
501  CGCCGGGCAA GCGGCCGTCC AGTCGTTAAT GTCGCGAGCG CCGGTCGCTC
551  CGGCAGCGGC ACCCGAACGT GCGCTAGCGT GGTTGATCGA ATCGCGTCGC
601  CGGGAGCACA GCGTCGCACT GCACCAGT
```

M. xenopi U4-U9 Length: 400 (SEQ ID NO 67)

```
  1  GTTCACCCAC CGCGAGCAAG CGGCGCCGGT AGAAGCTGCG ATGACACGCC
 51  AGTCGCCGCG AGACCCCCGC CGCCAGGTGC GCTAGCGTGG ATGGTCGAAT
101  CGCGTCGCAA CGCCTGCCCT GACAAGTCAC GGCGTTAATG GAGCGGTCCA
151  CGCAGCGTCG CGCGGAAGCG GCGCCCTGGG GATACAGCGT CGCAACACAG
```

```
201  TGGCGCCCCA ACGGCACTGA TGCACAGGAG AAGCCATGAC GTACTCGCCC
251  GGTAGCCCCG GATATCCACC CGCGCAGTCC CCCGGTTCCT ACGGCGGCTC
301  CCCACAGTCG TTCGCCAAAT CCGATGACGG CGCCAGCAAG CTGCAGCTGT
351  ATCTGACCGT CGCGGTGGTG GCGCTCGGCC TGGCGGCCTA CCTGGCGAGT
```

M. paratuberculosis U2-U1 Length: 707 (SEQ ID NO 68)

Underlined, the mutated nucleotidic base which allows to differentiate *M. Avium* from *M. Paratuberculosis*.

```
  1  TCGTAGCTGG CTTCCTCGTC GGTCCACAGC GCCCGCATCG CTTCCAGGTA
 51  TTCGCGCAGC ATGGTGCGGC GCCGGCCCGC CGGCACGCCG TGGTCGGCGA
101  GTTCGTCGGT GTTCCAGCCG AACCCGACGC CGAGGCTGAC CCGGCCGCCG
151  GACAGATGGT CAAGGGTGGC AATACTTTTC GCCAGCGTGA TCGGGTCGTG
```

Figure 3-continued

```
201  TTCGACCGGC AGGGCCACCG CGGTGGACAG CCGCACCCGC GAGGTGACGG
251  CACAGGCCGC GCCCAGACTG ACCCACGGGT CCAGGGTGCG CATGTAGCGG
301  TCGTCGGGCA GCGACGCGTC GCCGGTGGTC GGGTGCGCGG CCTCCCGCTT
351  GATCGGGATA TGCGTGTGTT CCGGCACGTA GAAGGTCGCA AACCCGTGGT
401  CGTCGGCAAG CTTCGCGGCC GCAGCCGGAG AGATGCCACG GTCGCTGGTG
451  AAAAGCACAA GCCCGTAATC CATGCAGTGA ATTAGAACGT GTTCTACCTC
501  TGCGGGGCAA GCTGTCGTGA TACGGACCGT CTCGCCGCGC GGTCGTCTGC
551  GAAGCCCGCG GGCAAGCCAA TGGCGACGGC ACCGGCCGTC GCACGTGCGC
601  TAGCGTGGGT GATCGACCGT GTCGCTCGCG CAGTGACGCG CCTGCAAGCA
651  CCGCGTCGCA TCGCAACCGT GGCGCCCGCT CGGCACTAAA AGGCAGTGGA
701  AGCAACA
```

M. marinum U2-U1 Length: 686 (SEQ ID NO 69)

This sequence is based on the sequence analysis of 6 different strains

```
  1  TCGTAGGCGG CTTCCTCCTG CGTCCACAGT CGCCCGCATC GCCTCGAGGT
 51  ATTCACGCAA CATCGTGCGG CGCCGTCCGG GTGGAACGCC ATGGTCGGCG
101  AGTTCGTCGG TGTTCCAACC GAACCCCACG CCGAGGCTGA CCCGTCCGCC
151  GGACAGATGA TCCAGCGTGG CAATGCTCTT GGCCAGGGTG ATCGGGTCAT
201  GCTCGACGGG CAGCGCCACC GCAGTCGACA GCCGTACCCG CGAGGTCACC
251  GCCGATGCCG CGCCCAAACT CACCCAGGGG TCCAGCGTGC GCATATAACG
```

```
301  ATCGTCGGGA AGCGAGGAAT CGCCCGTCGT TGGATGAGCG GCTTCTCGCT
351  TGATTGGGAT ATGGGTGTGC TCAGGCACGT AGAAGGTGTG AAAGCCGTGG
401  TCGTCAGCGA GTCTCGCCGC CGCCGCCGGA GCGATGCCGC GGTCGCTGGT
451  GAAAAGCACA AGCCCATAGT CCATAACAGA ATTAGAACGT GTTCTACCTC
501  GGCCGGGCAA GCGCCCCCCG CGCCAATCGG CTCGGCGGGA TCGACGGAGG
551  TGATGGCGCT GGTCGAGCGG GGGCAGGTCG CCGCGGCGCG AGCACCGGAA
601  CGTGCGCTAG CGTGGTTGTT CGAATCGCGT CGCAGGGACC AAGCGTCGCA
651  ATGCAGCAGC GGCGCCGCGA CGGCGCGCAA GTAACA
```

M. ulcerans U2-U1 Length: 685 (SEQ ID NO 70)

13 different strains have been sequenced.
These strains strains from Zaïre, Mexico, Surinam, Japan, Benin, Australia, Togo show a strong identity but disclose point mutations. There is therefore a certain degree of variations within an otherwise conserved sequence.
Primers are identical to those of *M. marinum* (both strains are indeed highly similar). The bases which are underlined are mutated nucleotidic bases but the base shown here is the most frequent among the sequenced species

```
  1  TCGTAGGCGG CTTCCTCCTG CGTCCACAGC GCCCGCATCG CCTCGAGGTA
 51  TTCACGCAAC ATCGTGCGGC GCCGTCCGGG TGGAACGCCA TGGTCGGCGA
```

Figure 3-continued

```
101  GTTCGTCGGT GTTCCAACCG AACCCCACGC CGAGGCTGAC CCGTCCGCCG
151  GACAGATGAT CCAGCGTGGC AATGCTCTTG GCCAGGGTGA TCGGGTCATG
201  CTCGACGGGC AGCGCCACCG CAGTCGACAG CCGTACCCGC GAGGTCACCG
251  CCGATGCCGC GCCCAAACTC ACCCAGGGGT CCAGCGTGCG CATATAACGA
301  TCGTCGGGAA GCGAGGAATC GCCCGTCGTT GGATGAGCGG CTTCTCGCTT
351  GATTGGGATA TGGGTGTGCT CAGGCACATA GAAGGTGTGA AAGCCGTGGT
401  CGTCAGCGAG TCTCGCCGCC GCCGCCGGAG CGATGCCGCG GTCGCTGGTG
451  AAAAGCACAA GCCCATAGTC CATAACAGAA TTAGAACGTG TTCTACCTCG
501  GCCGGGCAAG CGCCCCCCGC GCCAATCGGC TTGGCGGGAT CGACGGAGGT
551  GATGGCGCTG GTCGAGCGGG GGCAGGTCGC CGCGGCGCGA GCACCGGAAC
601  GTGCGCTAGC GTGGTTGTTC GAATCGCGTC GCAGGGACCA AGCGTCGCAA
651  TGCAGCAGCG GCGCCGCGAC GGCGCGCAAG TAACA
```

M. leprae U2-U1 Length: 729 (SEQ ID NO 71)

```
  1  TCATATAACG GCTTCATTCT TGTGTCCATA ATGCCTGCAT TGCTTCGAGG
 51  CATTCGTACA CCATGGTGCG GCGCCGCCCG GATGGCACAT CGTGATCGGT
101  GAGCTCGTTG GTCTTCCAAC CGAACCCGAC GCCGAAGTTC ACTCACTCGC
151  CGGACAAATT ATCCAGGTTG ACAATACTTT TCGCAAGTGT GATTGGGTCA
```

201 TGTTAGACGG GCAGCGCCAC CACCATGAAC AGTCGTAGCC TGCCGATATA
251 ACCCGCATGT CGCGCCCAAA CTTACCCATG AGTCATAGGT ACGCATCGCA
301 TATAGCTGTC GTCACTGGAC AGTGATACTC ATCCGTAACC AGGTAGTGGG
351 GTCTGAGTGG CAATGGCATA TGGGTGTGTT CGGGCACATA GAACTTGCGG
401 AAGCCGTGGC TCTCCGCAAG CTTGACTGCT GCCGCGGGGG TGATGCCGCG
451 GTCGTTGGTT AAAAGCGCAA TCCCGTAGCC CATACCAAGA ATTTAGAGCG
501 TGTTCCACCT GCGACGGCCA AGCGGTCGTG CCGACGATTT CGGCGTCCAT
551 CGGTGGTAGG CGAGCTGACA CGCAGGTCGT GCCGGCGCGG TCGCCCTAAC
601 GTGCGCTAGC GTTGATGATC GAATGCGCCG CAACGTAAGC GCTGCCAATT
651 TGGGCGTTTA TCCAACGGTG CGCATGGGAG CACAGCGTTG CACTGCAGCA
701 GTGGCGCCGT GACGGCACTG GAAATAACA

M. nonchromogenicum U4-U1 Length: 129 (SEQ ID NO 72)

1 GTTCCTGTTC GGCGGGCAAC GGGGGGGTCC TTGTCGCGCA GTGTTGACCC
51 ACCGACTCGG CCCGCAAGTG CGCTAGCGTG GATGGTCGAA GCGCGCCGCA
101 CCGCCCACCA GCGCCCTGCC ACAAGCACA

M. scrofulaceum U4-U1 Length: 219 (SEQ ID NO 73)

1 GTTCTACCTC CGGTGAGCAA GCTGCCGCCG CGGCGGCACG GATCGGCGTC
51 CAAGCCGGTC GCGACGGCAC GCCCGTCCCG AAGTGCGCTA GCGTGGTTGA
101 TCGATCGCGT CGCAACGCAA CCGCCGGGCA CGGCATTCGT GGAACGGCGC

Figure 3-continued

151 GCCCGCACGC ACAGCGCCGC GACGCAACTG TGGCGCCCGC AAAGGCACTT
201 CACGGCACTG GAAGCAACA

M. triplex U4-U1 Length: 116 (SEQ ID NO 74)

1 GTTCTACCTT GGTCGGCAAG CGGCGCGGGA ACGGCCCCGG CACCGGCTCC
51 CCGACGTGCG CTAGCGTGGT TGTTCGAATC GCGTCGCAAC GCAAGCGCGG
101 CGAGCCTGGA AAAACA

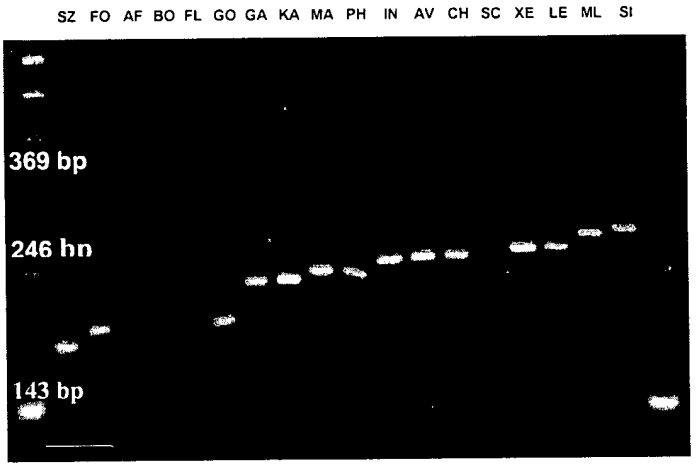
M. Paratuberculosis F57 sequence

M. paratuberculosis F57b - MPT1 Length: 618 (SEQ ID NO 75)

1 GATCTCAGAC AGTGGCAGGT GGCGGCTCCG AAGCTGGCGT CAGCTATTGG
51 TGTACCGAAT GTTGTTGTCA CCGAGCCGGT CCCAGGTGTG TTCGAGTTGC
101 AGCTGAGAAT TGTCGATCCG CTTAGTTCGC CGCTTGAATG GTCGTCTGTG

151 CCAGCCGCCC ACTCGTGGTC TCTGAGTTTG GGTATCGATG AAATGGGCGT
201 CTACCAGTCG CTCCCGTTGG CGAACGTATC GGGCGTTGTA GTGGGAGGCG
251 TACCAGGGTC GGGGAAAACC GCGTGGCTGA CGAGTGCTCT GGGGTCGTTC
301 GGTGCGTCAG CGGCGGTCCA GTTCGCTGTC ATCGACGGGA AGGGTGGTCA
351 GGACTTGGAA TGCCTGCGTG CTCGTAGCTG CCGATTCATG AATGACGATC
401 TGGAGCTGCC TGAGATTGCA GCGATTCTGA ATGACGCGAC CGGTCTAGTC
451 CGTGATCGAA TTAGACAGGG CAACAACATA TTCGGATCGT CCAACTTTTG
501 GGATCGCGGC CCGACGCCGC AGGTTCCGCT GGTGTTCGTG GTGATTGACG
601 GCTATCGGGG CCGAGATC

Figure 4. U1-U4 consensus amplification of us-p34 regions of different mycobacterial species



SZULGAI : 163 pb

FORTUITUM : 177 pb
AFRICANUM : 178 pb
BOVIS / TUB. : 178 pb
FLAVESCENS : 178 pb
GORDONAE : 182 pb

GASTRI : 223 pb
KANSASII : 225 pb

MARINUM : 236 pb
PHLEI : 236 pb

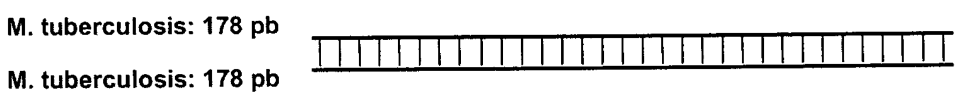
INTRACELLULARE : 255 pb
AVIUM / PARATUB. : 257 pb
CHELONAE : 256 pb
SCROFULACEUM : 259 pb

XENOPI : 265 pb
LEPRAE : 269 pb

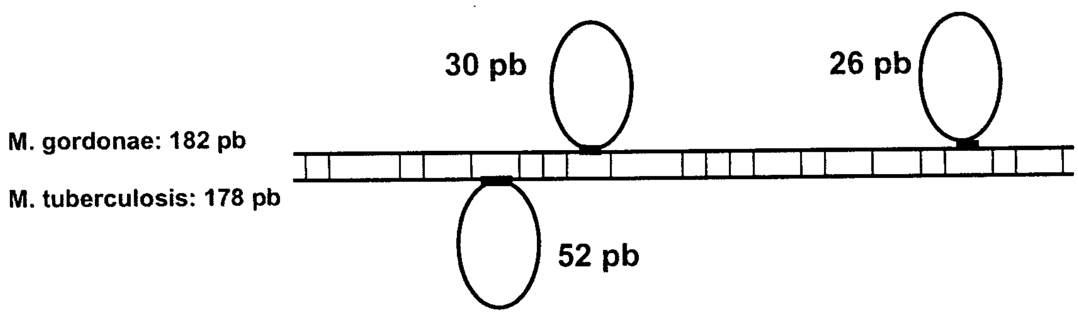
MALMOENSE : 290 pb
SIMIAE : 298 pb

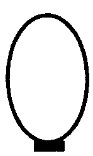
Figure 5. Specific and non specific hybidization

Homologous hybridization between both 178-bp amplicons from M. tuberculosis



Deletion within each of both single strands hampers hybridization between the 182-bp amplicon from M. gordonae and the 178-bp amplicon from M. tuberculosis





Schematic representation of a deletion

Figure 6. Differential reverse hybridization of mycobacteria target amplicons on a nylon membrane disclosing species-specific mycobacteria probes.
a) Unlabeled amplified DNA segments specific for various mycobacteria species were first transferred on nylon membrane *(M. tuberculosis* (TB), *M. avium* (AV), *M. szulgai* (SZ), *M. kansasii* (KA), *M. xenopi* (XE), *M. simiae* (SI) and *M. malmoense* (ML)).
b) Digoxigenin-labeled amplicons from *M. tuberculosis* (TB*), *M. avium* (AV*), *M. szulgai* (SZ*), *M. kansasii* (KA*), *M. xenopi* (XE*) and *M. simiae* (SI*) were hybridized on the nylon membrane. Specific differential hybridization is obtained.

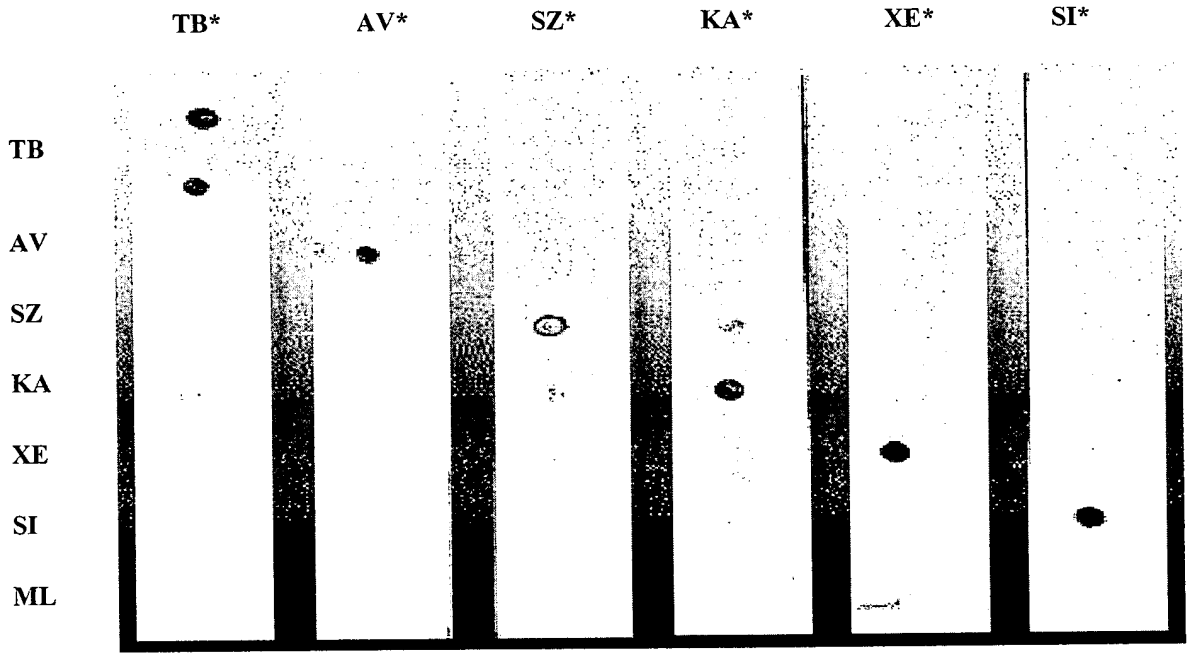
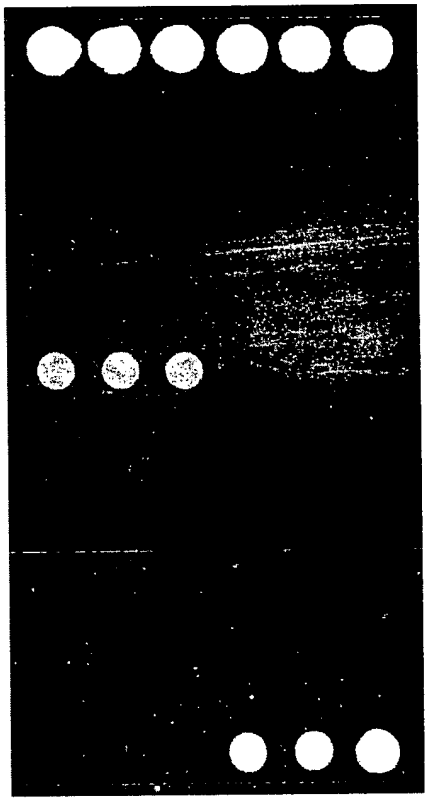


Figure 7. Example of biochips detecting specifically *M. gordonae*.

Control of fixation



Control of hybridization

Figure 8. Alignment of several Mycobacterial us-p34 sequences.

Paramaters used for sequence alignement:
gap creation penalty = 5; gap extension penalty = 1

```
          1                                                        50
{mycAV21}  tcgtag.ctg gcttcctcgt cggtccacag .cgc-cg-at c-cttccagg
{mycPT2Z}  tcgtag.ctg gcttcctcgt cggtccacag .cgc-cg-at c-cttccagg
{mycML2Z}  tcgtag.gcc gcttcctcct gggtccacag .cgc-cg-at t-cctcgatg
{mycSI2Z}  tcgtat.tgg gcttcttcct gcgtccacag .cgc-cg-at g-cttccagg
{mycTB21}  tcatag.cag gcctcctctt gggtccaca. acgc-cg-at c-cctcgagg
{mycBO2Z}  tcatag.cag gcctcctctt gggtccaca. acgc-cg-at c-cctcgagg
{mycMA2Z}  tcgtag.gcg gcttcctcct gcgtccacag tcgc-cg-at c-cctcgagg
{mycUL2Z}  tcgtag.gcg gcttcctcct gcgtccacag .cgc-cg-at c-cctcgagg
{mycGA3Z}  gtg..... ..... ..... ....-gc-gg c-ccccggcg
{mycKA31}  gtg..... ..... ..... ....-gc-gg c-c.......
{mycGO31}  gtg..... ..... ..... ....-ga-ga c-g.......
{mycSZ31}  gtg..... ..... ..... ....-gg-gg c-c.......
{mycLE2Z}  tcatataacg gcttcattct tgtgtccata atgc-tg-at t-cttcgagg
Consensus  ---------- ---------- ---------- ----C--C-- -G--------

          51                                                       100
{mycAV21}  tattcgcgca gcatggtgcg gcgccggc-c -ccg-c--gc cg--g--ggc
{mycPT2Z}  tattcgcgca gcatggtgcg gcgccggc-c -ccg-c--gc cg--g--ggc
{mycML2Z}  tattcacgca gcatggtgcg acggcgcc-g -ccg-c--gc cg--g--ggc
{mycSI2Z}  tactcgcgca gcatggtccg ccggcgcg-c -gcg-c--gt tg--g--ggc
{mycTB21}  tattcgcgca gcatggtgcg gcggcgtc-g -gtg-c--ac ca--a--gac
{mycBO2Z}  tattcgcgca gcatggtgcg gcggcgtc-g -gtg-c--ac ca--a--gac
{mycMA2Z}  tattcacgca acatcgtgcg gcgccgtc-g -gtg-a--gc ca--g--ggc
{mycUL2Z}  tattcacgca acatcgtgcg gcgccgtc-g -gtg-a--gc ca--g--ggc
{mycGA3Z}  gcacgccatg gtcggcgagt tcgtgcgc-c -gcg-c--gc ca--g--ggc
{mycKA31}  ..... ..... .....g-c -gcg-c--gc ca--g--agc
{mycGO31}  ..... ..... .....c-g -cca-c--gt ta--g--ggc
{mycSZ31}  ..... ..... .....c-g -ccg-g--gc cg--a--agc
{mycLE2Z}  cattcgtaca ccatggtgcg gcgccgcc-g -atg-c--at cg--a--ggt
Consensus  ---------- ---------- --------C- G---G-AC-- --TG-TC---

          101                                                      150
{mycAV21}  g--t----c- --g-----g- -g--c--g-- g--g-ggc-g --c-ggccgc
{mycPT2Z}  g--t----c- --g-----g- -g--c--g-- g--g-ggc-g --c-ggccgc
{mycML2Z}  g--c----c- --g-----g- -a--c--a-- g--g-ggc-g --c-ggccgc
{mycSI2Z}  c--t----c- --g-----a- -g--c--g-- g--c-cac-g --c-gtccgc
{mycTB21}  g--c----c- --g-----g- -g--c--g-- c--g-cgc-g --c-ggccgt
{mycBO2Z}  g--c----c- --g-----g- -g--c--g-- c--g-cgc-g --c-ggccgt
{mycMA2Z}  g--t----c- --g-----a- -g--c--c-- g--g-ggc-g --c-gtccgc
{mycUL2Z}  g--t----c- --g-----a- -g--c--c-- g--g-ggc-g --c-gtccgc
{mycGA3Z}  g--t----c- --g-----g- -g--t--g-- g--g-cgc-g --c-ggcccc
{mycKA31}  g--t----c- --g-----g- -g--t--g-- g--g-cgc-g --c-gccccc
{mycGO31}  g--c----c- --g-----g- -g--c--g-- g--g-ggc-a --t-gcccgc
{mycSZ31}  g--c----c- --a-----g- -g--g--g-- g--g-ggc-g --c-ggctgc
{mycLE2Z}  g--c----t- --c-----a- -g--c--g-- g--g-agt-c --t-actcgc
```

```
Consensus   -AG-TCGT-G GT-TTCCA-C C-AA-CC-AC -CC-A---T- AC-C------
```

Figure 8- continued

```
                151                                                200
{mycAV21}   cg--c-ga-g g--a-ggg-g g-a--a--t- -c--c-gc-- ---c--g--g
{mycPT2Z}   cg--c-ga-g g--a-ggg-g g-a--a--t- -c--c-gc-- ---c--g--g
{mycML2Z}   cg--c-gg-g g--c-agg-g g-a--a--t- -c--c-gc-- ---c--g--g
{mycSI2Z}   cg--c-ga-g g--c-ggg-g g-g--g--t- -c--c-gc-- ---c--g--g
{mycTB21}   gc--c-aa-g a--c-gcg-c g-a--g--t- -c--c-gc-- ---c--a--a
{mycBO2Z}   gc--c-aa-g a--c-gcg-c g-a--g--t- -c--c-gc-- ---c--a--a
{mycMA2Z}   cg--c-ga-g a--c-gcg-g g-a--g--c- -g--c-gg-- ---c--g--a
{mycUL2Z}   cg--c-ga-g a--c-gcg-g g-a--g--c- -g--c-gg-- ---c--g--a
{mycGA3Z}   cg--t-.g-g g--c-gcg-g g-a--g--t- -g--c-gc-- ---c--g--a
{mycKA31}   cg--t-gg-g g--c-gcg-g g-a--g--t- -g--c-gc-- ---c--g--a
{mycGO31}   cg--c-gg-g a--c-gcg-g g-g--g--t- -c--c-ag-- ---c--g--a
{mycSZ31}   cg--c-ga-g a--c-gcg-g g-a--g--t- -g--c-gc-- ---c--a--a
{mycLE2Z}   cg--c-aa-t a--c-ggt-g a-a--a--t- -c--a-gt-- ---t--g--a
Consensus   --GA-A--T- -TC-A---T- -C-AT-CT-T T-GC-A--GT GAT-GG-TC-
```

```
               201                                                250
{mycAV21}   --t-cg--cg ---gg--c-- cg-gg-ggac -gc-gc-cc- .-cgaggtg-
{mycPT2Z}   --t-cg--cg ---gg--c-- cg-gg-ggac -gc-gc-cc- .-cgaggtg-
{mycML2Z}   --c-cg--gg ---gc--c-- cg-gg-agac -gc-gc-cc- .-cgacgtc-
{mycSI2Z}   --c-cg--gg ---gc--g-- cg-gg-ggac -gt-gc-cc- .-cgaggtg-
{mycTB21}   --c-cg--cg ---gc--c-- cg-gg-ggca -gc-gg-tc- .-cgacgtc-
{mycBO2Z}   --c-cg--cg ---gc--c-- cg-gg-ggca -gc-gg-tc- .-cgacgtc-
{mycMA2Z}   --c-cg--gg ---gc--c-- cg-ag-cgac -gc-gt-cc- .-cgaggtc-
{mycUL2Z}   --c-cg--gg ---gc--c-- cg-ag-cgac -gc-gt-cc- .-cgaggtc-
{mycGA3Z}   --c-cc--c. ---gc--a-- cg-gg-tgac -gc-tg-ct- .-ggaggtg-
{mycKA31}   --c-cg--cg ---ac--a-- cg-tg-tgac -gt-gg-cc- .-gaaggtg-
{mycGO31}   --c-cg--cg ---ac--g-- tg-cg-cgac -gc-gc-cc- .-cgacgtc-
{mycSZ31}   --c-cg--cg ---gc--c-- cg-gg-ggac -ac-gg-cc- .-agacgtc-
{mycLE2Z}   --t-ag--gg ---gc--c-- ca-ca-gaac -gt-gt-gc- t-ccgatat-
Consensus   TG-T--AC-- GCA--GC-AC --C--T---- A--C--A--C -G-------A
```

```
               251                                                300
{mycAV21}   cgg-acag-c c--g----ga --g-----c- gg--cagg-- .....g----
{mycPT2Z}   cgg-acag-c c--g----ga --g-----c- gg--cagg-- .....g----
{mycML2Z}   cgg-gcac-c c--g----gg --c-----c- gg--tagc-- .....g----
{mycSI2Z}   ccg-gcac-c c--g----ga --g-----c- gg--cagc-- .....g----
{mycTB21}   ccg-cgat-c t--t----gg --c-----c- gg--caac-- .....g----
{mycBO2Z}   ccg-cgat-c t--t----gg --c-----c- gg--caac-- .....g----
{mycMA2Z}   ccg-cgat-c c--g----aa --c-----g- gg--cagc-- .....g----
{mycUL2Z}   ccg-cgat-c c--g----aa --c-----g- gg--cagc-- .....g----
{mycGA3Z}   ccg-tgaa-c c--a----ag --c-----c- gg--cagg-- .....g----
{mycKA31}   ccg-tgaa-c c--g----aa --c-----c- gg--cagc-- .....g----
{mycGO31}   cag-acac-c c--g----gg --c-----g- ga--cagg-- .....g----
```

```
{mycSZ31}  ccg-ggcc-c a--a----aa --c-----c- gg--cagc-- .....g----
{mycLE2Z}  acc-gcat-t c--g----aa --t-----t- ag--atag-- acgcat----
Consensus  ---C----G- -GC-CCCA-- CT-ACCCA-G --TC----GT ------CGCA
```

Figure 8- continued

```
           301                                                350
{mycAV21}  -g--g-gg-- g--gggc.-g c-a.cgcgt- gccg-tggtc g-g-gcgcg-
{mycPT2Z}  -g--g-gg-- g--gggc.-g c-a.cgcgt- gccg-tggtc g-g-gcgcg-
{mycML2Z}  -a--g-gg-- g--cggca-g c-a.cgcgc- accc-tcgtc g-a-gggcc-
{mycSI2Z}  -g--g-gg-- g--gggc.-g c-a.ttcgt- gccc-tcgtg g-a-gggcc-
{mycTB21}  -a--g-gg-- g--cggc.-g c-a.agcgt- accc-tcgtc g-a-gggcc-
{mycBO2Z}  -a--g-gg-- g--cggc.-g c-a.agcgt- accc-ccgtc g-a-gggcc-
{mycMA2Z}  -a--a-ga-- g--ggga.-g c-a.ggaat- gccc-tcgtt g-a-gagcg-
{mycUL2Z}  -a--a-ga-- g--ggga.-g c-a.ggaat- gccc-tcgtt g-a-gagcg-
{mycGA3Z}  -a--g-gg-- g--cggc.-g c-a.cgcgt- accc-tcgtg g-a-gggcg-
{mycKA31}  -a--g-gg-- g--cggc.-g c-a.cgcgt- accc-tcgtg g-a-.ggcg-
{mycGO31}  -a--a-gg-- g--gggc.-g c-t.ctcgt- tccg-tggtg g-a-gagcc-
{mycSZ31}  -g--g-gg-- a--gggc.-g c-a.cgcgt- actc-tagtg g-a-gggca-
{mycLE2Z}  -a--g-tg-- g--actgg-c a-tgatact- atcc-taacc a-g-agtgg-
Consensus  T-TA-C--TC -TC-----A- -G-------C ----G----- -G-T-----G
```

```
           351                                                400
{mycAV21}  cctccc-ctt g-tc--g--a --c-----t- -c--c--g-- g-agg-cgca
{mycPT2Z}  cctccc-ctt g-tc--g--a --c-----t- -c--c--g-- g-agg-cgca
{mycML2Z}  cctcgc-ctt g-cc--g--a --g-----t- -c--c--g-- g-acg-ctgg
{mycSI2Z}  cctcgc-ctt g-tc--g--g --a-----t- -t--c--g-- g-acg-tgtg
{mycTB21}  cctggc-ctt g-cc--g--g --g-----t- -g--c--g-- a-acg-gcga
{mycBO2Z}  cctggc-ctt g-cc--g--g --g-----t- -g--c--g-- a-acg-gcga
{mycMA2Z}  cttctc-ctt g-tt--g--a --g-----c- -a--c--g-- g-agg-gtga
{mycUL2Z}  cttctc-ctt g-tt--g--a --g-----c- -a--c--a-- g-agg-gtga
{mycGA3Z}  cttccc-ttt g-cc--g--a --c-----t- -g--c--g-- g-gag-gcga
{mycKA31}  cctccc-ttt g-cc--g--g --c-----t- -g--c--g-- g-aag-gcga
{mycGO31}  cctcgc-ttt g-tc--g--a --c-----t- -g--t--g-- g-agg-gtga
{mycSZ31}  cctccc-ctt g-tc--g--g --g-----t- -a--c--g-- g-acg-ctga
{mycLE2Z}  gtctga-tgg c-at--c--a --g-----t- -g--c--a-- g-act-gcgg
Consensus  ------G--- -A--GG-AT- TG-GTGTG-T C-GG-AC-TA -A---T----
```

```
           401                                                450
{mycAV21}  --c--g--gt cg--g--a-- ct-cg-g--c --a--c--a- ag--g--a--
{mycPT2Z}  --c--g--gt cg--g--a-- ct-cg-g--c --a--c--a- ag--g--a--
{mycML2Z}  --g--g--gt cg--g--a-- tt-gg-g--t --c--c--g- ag--g--g--
{mycSI2Z}  --g--a--gt cg--g--g-- tt-gg-c--g --c--c--g- cg--g--c--
{mycTB21}  --c--g--gc tt--a--a-- tc-gg-g--c --g--c--g- tg--g--g--
{mycBO2Z}  --c--g--gc tt--a--a-- tc-gg-g--c --g--c--g- tg--g--g--
{mycMA2Z}  --g--g--gt cg--a--g-- tc-cg-c--c --c--c--a- cg--g--g--
```

```
{mycUL2Z}  --g--g--gt cg--a--g-- tc-cg-c--c --c--c--a- cg--g--g--
{mycGA3Z}  --g--a--gt cg--g--c-- tt-cg-g--t --c--c--g- ag--c--a--
{mycKA31}  --g--a--gt cg--g--c-- tt-cg-g--t --c--g--a- aa--g--a--
{mycGO31}  --a--a--tg tg--g--a-- tt-cg-t--t --c--a--g- aa--a--g--
{mycSZ31}  --a--g--gt cg--g--c-- ct-tg-g--c --c--c--g- ca--g--g--
{mycLE2Z}  --g--g--gc tc--c--a-- ct-ga-t--t --c--g--g- tg--g--g--
Consensus  AA-CC-TG-- --TC-GC-AG --T--C-GC- GC-GC-GG-G --AT-CC-CG
```

Figure 8- continued

```
          451                                                    500
{mycAV21}  g--gc----g --a--ca-a- gc-cg--atc ---gcagtg- a.-----a--
{mycPT2Z}  g--gc----g --a--ca-a- gc-cg--atc ---gcagtg- a.-----a--
{mycML2Z}  g--gc----g --a--ta-a- gc-cg--atc ---ggacag- a.-----a--
{mycSI2Z}  a--ac----g --a--ca-g- gc-cg--atc ---gcacag- a.-----a--
{mycTB21}  g--gc----g --c--ca-a- gt-cg--gtg ---gcaccg- a.-----a--
{mycBO2Z}  g--gc----g --c--ca-a- gt-cg--gtg ---gcaccg- a.-----a--
{mycMA2Z}  g--gc----g --a--ca-a- gc-ca--gtc ---.aacag- a.-----a--
{mycUL2Z}  g--gc----g --a--ca-a- gc-ca--gtc ---.aacag- a.-----a--
{mycGA3Z}  g--gc----g --a--ga-a- gc-cg--atc ---gaacag- a.-----a--
{mycKA31}  g--gc----g --a--ga-a- gc-cg--atc ---gaacag- a.-----a--
{mycGO31}  a--gc----g --c--aa-g- gg-tg--gtc ---gcccca- t.-----a--
{mycSZ31}  a--gc----g --a--ta-a- gc-cg--atc ---gcaccg- a.-----a--
{mycLE2Z}  g--gt----t --a--cg-a- tc-cg--gcc ---accaag- at-----g--
Consensus  -TC--TGGT- AA-AG--C-A --C--TA--- CAT------A --TTAGA-CG
```

```
          501                                                    550
{mycAV21}  -----t--ct ct-cggggca agctgtcgtg atacggaccg tctcgccgcg
{mycPT2Z}  -----t--ct ct-cggggca agctgtcgtg atacggaccg tctcgccgcg
{mycML2Z}  -----t--cg gc-gtgggca agccgctgcg ccgccgagga tctcgactcg
{mycSI2Z}  -----t--ct ct-tggagca agcggccccc gctacgtcga cccgcagacg
{mycTB21}  -----c--ct gc-ccgggca agcggcc... .......... ..........
{mycBO2Z}  -----c--ct gc-ccgggca agcggcc... .......... ..........
{mycMA2Z}  -----t--ct cg-ccgggca agcgcccccc gcgccaatcg gctcggcggg
{mycUL2Z}  -----t--ct cg-ccgggca agcgcccccc gcgccaatcg gcttggcggg
{mycGA3Z}  -----t--ct cc-ccgggca agcggctcat ctgccga... tcggcagcgg
{mycKA31}  -----t--ct ca-ccgggca agcggctcat ccgccgatcg tcggcagtgg
{mycGO31}  -----t--tt tt-gccg... .......... .......... ........ca
{mycSZ31}  -----t--.. ct-cgat... .......... .......... ........ga
{mycLE2Z}  -----c--ct gc-acggcca agcggtcgtg ccgacgattt cggcgtcc..
Consensus  TGTTC-AC-- --G------- ---------- ---------- ----------
```

```
          551                                                    600
{mycAV21}  .......... .cggtcgtct ccgaagcccg cgggcaagcc aa-ggcgacg
{mycPT2Z}  .......... .cggtcgtct gcgaagcccg cgggcaagcc aa-ggcgacg
```

```
{mycML2Z}  gacccacaac actggtcggc gccgggcgcg ccgacaggtc gg-cggcccg
{mycSI2Z}  ggccgctgag ac.gatcgct cctggtcgcg cctaggggcc gg-cgctccc
{mycTB21}  .......... ....gtccag tcgttaatgt cgcgagcgcc gg-cgctccg
{mycBO2Z}  .......... ....gtccag tcgttaatgt cgcgagcgcc gg-cgctccg
{mycMA2Z}  atc....gac ggaggtgatg gcgctggtcg agcgggggca gg-cgccgcg
{mycUL2Z}  atc....gac ggaggtgatg gcgctggtcg agcgggggca gg-cgccgcg
{mycGA3Z}  .......... ...tgccggg gccggtatcg cgggcggcaa gg-cgccacg
{mycKA31}  .......... ...tgacggg gccggtatca cggg.ggcaa gg-cgccacg
{mycGO31}  .......... ...gccgacc ccctgcggcg acgggcacta gt-gtcagag
{mycSZ31}  .......... ...gcaagcg gcccggtcgg ccgacgagca gg-cggcccg
{mycLE2Z}  .......... ....atcggt ggtaggcgag ctgacacgca gg-cgtgccg
Consensus  ---------- ---------- ---------- ---------- --T-------
```

Figure 8- continued

```
          601                                                   650
{mycAV21}  -caccggccg tcgcac-tg- -cta----g- gtgat--acc gtgtcgc...
{mycPT2Z}  -caccggccg tcgcac-tg- -cta----g- gtgat--acc gtgtcgc...
{mycML2Z}  -cacgggcgg ccgaac-tg- -cta----g- gtgat--atc gcgtcgcaac
{mycSI2Z}  -cgcacccgc tcgaac-tg- -cta----g- ttgat--gtc gcg.cgtaac
{mycTB21}  -cagcggcac ccgaac-tg- -cta----g- ttgat--a.. ..........
{mycBO2Z}  -cagcggcac ccgaac-tg- -cta----g- ttgat--a.. ..........
{mycMA2Z}  -cgcgagcac cggaac-tg- -cta----g- ttgtt--a.. ..........
{mycUL2Z}  -cgcgagcac cggaac-tg- -cta----g- ttgtt--a.. ..........
{mycGA3Z}  -cgtgagtac ccggcc-tg- -cta----g- gtcat--a.. ..........
{mycKA31}  -cgcgagtac caggcc-tg- -cta----g- gtcat--a.. ..........
{mycGO31}  -tgcgctagc gtggtt-at- -aat----c- caggc--t.. ..........
{mycSZ31}  -cgcgaccag cagaac-tg- -cta----g- ttgat--a.. ..........
{mycLE2Z}  -cgcggtcgc cctaac-tg- -cta----t- atgat--aat gcgccgcaac
Consensus  G--------- ------G--C G---GCGT-G -----CG--- ----------
```

```
          651                                                   700
{mycAV21}  .......... .......... ....tcgcgc agtgacgcgc ctgcaagcac
{mycPT2Z}  .......... .......... ....tcgcgc agtgacgcgc ctgcaagcac
{mycML2Z}  gcaagatctc gaaggtgttt tcaaaggcgg cgcg.....c ctggaagtgc
{mycSI2Z}  gcaaacgcgg gcacgccctg gcgtcaccga cgggcgagcc ctgcagacac
{mycTB21}  .......... .......... .......... .atcgcgtcg ccgggagcac
{mycBO2Z}  .......... .......... .......... .atcgcgtcg ccgggagcac
{mycMA2Z}  .......... .......... .......... .atcgcgtcg cagggacca.
{mycUL2Z}  .......... .......... .......... .atcgcgtcg cagggacca.
{mycGA3Z}  .......... .......... .......... .......... ........at
{mycKA31}  .......... .......... .......... .......... ........at
{mycGO31}  .......... .......... .......... .......... ........ac
{mycSZ31}  .......... .......... .......... .......... ........gt
{mycLE2Z}  gtaagcgctg cca.atttgg gcgtttatcc aacggtgcgc atgggagcac
Consensus  ---------- ---------- ---------- ---------- ----------
```

```
           701                                                    750
{mycAV21}  c-cgtcgcat cgcaac.... .cgtggcgcc cgctcggcac taaaaggcag
{mycPT2Z}  c-cgtcgcat cgcaac.... .cgtggcgcc cgctcggcac taaaaggcag
{mycML2Z}  a-cgtcgcgc cgcaaatgcg gcgtcgc... ..tgagggtc ttgaaggcac
{mycSI2Z}  g-cgtcgcac tgcagcagtg acgtcgcgcc cgacgaggtc ttgaaggcac
{mycTB21}  a-cgtcgcac tgcaccag.. .......... .......... ..........
{mycBO2Z}  a-cgtcgcac tgcaccag.. .......... .......... ..........
{mycMA2Z}  a-cgtcgcaa tgcagcagcg gcgccgcgac ggcgc..... ..........
{mycUL2Z}  a-cgtcgcaa tgcagcagcg gcgccgcgac ggcgc..... ..........
{mycGA3Z}  t-tgtcgcag ggagcaatcg tcgcattgca gcaggcg.ta gcgacggcac
{mycKA31}  c-tgtcgcag ggagcaatcg tcgcattgca gcaggcg.ta gcgacggcac
{mycGO31}  c-cgtcgtgc cgaagcagag gggccgtgac ggcaccg... ..........
{mycSZ31}  c-c....... .......... gcaccggaaa gcaaccg... ..........
{mycLE2Z}  a-cgttgcac tgcagcagtg gcgccgtgac .......... .....ggcac
Consensus  -G-------- ---------- ---------- ---------- ----------
```

Figure 8- continued

```
           751                           782
{mycAV21}  tggaagcaac a------gcc ---------t -t
{mycPT2Z}  tggaagcaac a------gcc ---------t -.
{mycML2Z}  tggaagcaat a------gcc ---------t -.
{mycSI2Z}  tggaagcaac a------gcc ---------t -.
{mycTB21}  .......... t------gcc ---------t -g
{mycBO2Z}  .......... t------gcc ---------t -.
{mycMA2Z}  .gcaagtaac a------gcc ---------t -.
{mycUL2Z}  .gcaagtaac a------gcc ---------t -.
{mycGA3Z}  cggaggtaac a------gcc ---------t -.
{mycKA31}  tggaggtaac a------gcc ---------t -.
{mycGO31}  .gaagcaa.c a------ctt ---------c -g
{mycSZ31}  .gaagtaatc a------gcc ---------t -g
{mycLE2Z}  tggaaataac a------gcc ---------t -.
Consensus  ---------- -GGAGGA--- ATGACCTAC- C-
```

Figure 9. Alignment of three Mycobacterial us-p34 sequences (M. tuberculosis, M. avium and M. intracellulare.

Paramaters used for sequence alignement :
gap creation penalty = 5 ; gap extension penalty = 1

```
          1                                                                    60
{mycTB21}  tcatagcagg cctcctcttg ggtccacaac gcccgcatcg cctcgaggta ttcgcgcagc
{mycAV21}  tcgtagctgg cttcctcgtc ggtccacagc gcccgcatcg cttccaggta ttcgcgcagc
{mycIN4Z}  .......... .......... .......... .......... .......... ..........
Consensus  ---------- ---------- ---------- ---------- ---------- ----------

         61                                                                   120
{mycTB21}  atggtgcggc ggcgtccggg tggcacacca tgatcgacga gctcgtcggt gttccagccg
{mycAV21}  atggtgcggc gccggcccgc cggcacgccg tggtcggcga gttcgtcggt gttccagccg
{mycIN4Z}  .......... .......... .......... .......... .......... ..........
Consensus  ---------- ---------- ---------- ---------- ---------- ----------

        121                                                                   180
{mycTB21}  aacccgaccc cgacgctgac ccggccgtgc gacaaatgat ccagcgtcgc aatgcttttc
{mycAV21}  aacccgacgc cgaggctgac ccggccgccg gacagatggt caagggtggc aatacttttc
{mycIN4Z}  .......... .......... .......... .......... .......... ..........
Consensus  ---------- ---------- ---------- ---------- ---------- ----------

        181                                                                   240
{mycTB21}  gccagcgtga tcggatcatg ctcgaccggc agcgccaccg cggtggcaag ccggatccgc
{mycAV21}  gccagcgtga tcgggtcgtg ttcgaccggc agggccaccg cggtggacag ccgcacccgc
{mycIN4Z}  .......... .......... .......... .......... .......... ..........
Consensus  ---------- ---------- ---------- ---------- ---------- ----------

         241                                                                  300
{mycTB21}  gacgtcaccg ccgatgctgc tcccaggctc acccacgggt ccaacgtgcg catatagcgg
{mycAV21}  gaggtgacgg cacaggccgc gcccagactg acccacgggt ccagggtgcg catgtagcgg
{mycIN4Z}  .......... .......... .......... .......... .......... ..........
Consensus  ---------- ---------- ---------- ---------- ---------- ----------

         301                                                                  360
{mycTB21}  tcgtccggca gcgaagcgtc acccgtcgtc ggatgggccg cctggcgctt gaccgggatg
{mycAV21}  tcgtcgggca gcgacgcgtc gccggtggtc gggtgcgcgg cctcccgctt gatcgggata
{mycIN4Z}  .......... .......... .......... .......... .......... ..........
Consensus  ---------- ---------- ---------- ---------- ---------- ----------

        361                                                                   420
{mycTB21}  tgggtgtgtt cgggcacgta aaacgtgcga aacccgtggc tttcagcaag tctggcggcc
{mycAV21}  tgcgtgtgtt ccggcacgta gaaggtcgca aacccgtggt cgtcggcaag cttcgcggcc
{mycIN4Z}  .......... .......... .......... .......... .......... ..........
Consensus  ---------- ---------- ---------- ---------- ---------- ----------

        421                                                                   480
{mycTB21}  gcggccgggg tgatgccgcg gtcgctggtg aacagcacaa gtccgtagtg catgcaccga
{mycAV21}  gcagccggag agatgccacg gtcgctggtg aaaagcacaa gcccgtaatc catgcagtga
{mycIN4Z}  .......... .......... .......... .......... .......... ..........
Consensus  ---------- ---------- ---------- ---------- ---------- ----------

        481                                                                   540
{mycTB21}  attagaacgt ----c----g c--c-g---- --ggcc--cc agtc-ttaa- g---------
{mycAV21}  attagaacgt ----t----c t--g-g---- --tgtc--ga tacg-accg- c----cgcgc
{mycIN4Z}  .......... ----t----g t--t-a---- --tccg--ga tacc-accg- c----cggag
Consensus  ---------- GTTC-ACCT- -GC-G-GCAA GC----GT-- ----G----T -TCGC-----

        541                                                                   600
```

```
{mycTB21}  .......... .......... .gagc-c-gg -c--tc--g- -g---cacc- -a--------
{mycAV21}  ggtcgtctcc gaagcccgcg ggcaa-c-aa -g--ga--g- -c---ccgt- -c--------
{mycIN4Z}  ggccgccggg ggcctcgccg cccaa-a-ag -g--gg--c- -c---ttcc- -c--------
Consensus  ---------- ---------- -----G-C-- T-GC--CG-C A-CGG----C G-ACGTGCGC


        601                                                                660
{mycTB21}  --------t- -----..... .......... .aa-cg--tc g-c-gg---- -a--------
{mycAV21}  --------g- -----accgt gtcgctcgcg cag-ga--cg c-t-ca---- -c--------
{mycIN4Z}  --------g- -----accgc gtcgc.aatg cgg-ga--cg c-t-ca---- -a--------
Consensus  TAGCGTGG-T GATCG----- ---------- ---T--CG-- -C-G--AGCA C-GCGTCGCA

         661                                                       720
{mycTB21}  ct--ac-a-t .......... .......... .......... .........--- ----------
{mycAV21}  tc--aa-c-t ggcgcccgct cggcactaaa aggcagtgga agcaaca--- ----------
{mycIN4Z}  tc--ca-c-c ggcgcccgct cggcacttaa aggcactggt agcaaca--- ----------
Consensus  --GC--C-G- ---------- ---------- ---------- -------GGA GGAGCCATGA

         721
{mycTB21}  -------g
{mycAV21}  -------t
{mycIN4Z}  -------.
Consensus  CCTACTC-
```

Figure 10. Alignment of several pairs of Mycobacterial us-p34 sequences.

Paramaters used for sequence alignement

gap creation penalty = 50 ; gap extension penalty = 3

M. Tuberculosis* x *M. Xenopi

Percent Similarity: 45.749 Percent Identity: 45.749

```
351 GACCGGGATGTGGGTGTGTTCGGGCACGTAAAACGTGCGAAACCCGTGGC 400
                                                  | |   |
  1 ....................................GTTCACCCACC 11

401 TTTCAGCAAGTCTGGCGGCCGCGGCCGGGGTGATGCCGCGGTCGCTGGTG 450
          |     | |||  |  || | | |||  |  | ||||| |
 12 GCGAGCAAGCGGCGCCGGTAGAAGCTGCGATGACACGCCAGTCGCCGCGA 61

451 AACAGCACAAGTCCGTAGTGCATGCACCGAATTAGAACGTGTTCCACCTG 500
     ||  |    | | |  | ||  ||   ||       |   |   | |
 62 GACCCCCGCCGCCAGGTGCGCTAGCGTGGATGGTCGAATCGCGTCGCAAC 111

501 CGCCGGGCAAGCGGCCGTCCAGTCGTTAATGTCGCGAGCGCCGGTCGCTC 550
     | |  |   |    |||  | ||||||||  |||  |  ||    ||
112 GCCTGCCCTGAC..AAGTCACGGCGTTAATGGAGCGGTCCACGCAGCGTC 159

551 CGGCAGCGGCACCCGAACGTGCGCTAGCGTGGTTGATCGAATCGCGTCGC 600
     || |  ||           ||   |  ||   |  |  ||||  | |
160 GCGCGGAAGC..........GGCGCCCTGGGGATACAGCGTCGCAACAC 198

601 CGGGAGCACAGCGTCGCACTGCACCAGTGGAGGAGCCATGACCTACTCG 649
     | |    |      ||||||   ||  |||| |||||||||  ||||||
199 AGTGGCGCCCCAACGGCACTGATGCACAGGAGAAGCCATGACGTACTCG 247
```

M. Tuberculosis* x *M. Gordonae

Percent Similarity: 69.795 Percent Identity: 69.795

```
 51 TTCGCGCAGCATGGTGCGGCGGCGTCCGGGTGGCACACCATGATCGACGA 100
               ||||| || || ||||   ||||   ||| ||| |||
  1 ............GTGCGACGACGGCCGGCCAGCACGTTATGGTCGGCGA 37

101 GCTCGTCGGTGTTCCAGCCGAACCCGACCCCGACGCTGACCCGGCCGTGC 150
    |||||||||||||||||||||||||| |||| ||| || || |||
 38 GCTCGTCGGTGTTCCAGCCGAACCCGACGCCGAGGCTAACTCGCCCGCCG 87

151 GACAAATGATCCAGCGTCGCAATGCTTTTCGCCAGCGTGATCGGATCATG 200
    ||||  |||||||||| || ||||||||||||  |||||||| |||||
 88 GACAGGTGATCCAGCGTGGCGATGCTTTTCGCCAAGGTGATCGGGTCATG 137
```

```
             .         .         .         .         .
201 CTCGACCGGCAGCGCCACCGCGGTGGCAAGCCGGATCCGCGACGTCACCG 250
    ||||||||||| ||| || || || |  ||||| | |||||||||||| |
138 CTCGACCGGCAACGCGACTGCCGTCGACAGCCGCACCCGCGACGTCACAG 187
```

Figure 10-continued

```
             .         .         .         .         .
251 CCGATGCTGCTCCCAGGCTCACCCACGGGTCCAACGTGCGCATATAGCGG 300
    |  | || || |||||||||||||| || ||||  ||||||||||| |||
188 CACACGCCGCGCCCAGGCTCACCCAGGGATCCAGGGTGCGCATATAACGG 237
             .         .         .         .         .
301 TCGTCCGGCAGCGAAGCGTCACCCGTCGTCGGATGGGCCGCCTGGCGCTT 350
    ||||| |||||||   |||| || || || ||||| ||||||| ||| ||
238 TCGTCGGGCAGCGTCTCGTCTCCGGTGGTGGGATGAGCCGCCTCGCGTTT 287
             .         .         .         .         .
351 GACCGGGATGTGGGTGTGTTCGGGCACGTAAAACGTGCGAAACCCGTGGC 400
    || |||||| || ||||||||||| ||||| || ||| |||| || ||
288 GATCGGGATATGCGTGTGTTCGGGTACGTAGAAGGTGTGAAAACCATGTG 337
             .         .         .         .         .
401 TTTCAGCAAGTCTGGCGGCCGCGGCCGGGGTGATGCCGCGGTCGCTGGTG 450
    | || |||||| | || || || || ||||  || ||||| |||||||||
338 TGTCGGCAAGTTTCGCTGCTGCCGCAGGGGAAATACCGCGATCGCTGGTG 387
             .         .         .         .         .
451 AACAGCACAAGTCCGTAGTGCATGCACCGAATTAGAACGTGTTCCACCT. 499
    ||||| || || | ||||| ||||| || | ||||||||||||| || |
388 AACAGAACGAGGCTGTAGTCCATGCCCCAATTTAGAACGTGTTCTACTTT 437
             .         .         .         .         .
500 ..GCGCCGGGCAAGCGGCCGTCCAGTCGTTAATGTCGCGAGCGCCGGTCG 547
      ||  | | | | |  | |    | ||   |      |   |  |  ||
438 TGGCCGCAGCCGACCCCCTGCGGCGACGGGCACTAGTTGTCAGAGGTGCG 487
             .         .         .         .         .
548 CTCCGGCAGCGGCACCCGAACGTGCGCTAGCGTGGTTGATCGAATCGCGT 597
    ||   |  |  |  |     |||       |||      |||   ||
488 CTAGCGTGGTTGATCGAATGCGTCGCAGGCCGTACCGCGTCGTGCCGAAG 537
             .         .         .         .         .
598 CGCCGGGAGCACAGCGTCGCACTGCACCAGTGGAGGAGCCATGACCTACT 647
    |   |||  |    || | |      | |  ||||||   |||||||||
538 CAGAGGGGCCGTGACGGCACCGGAAGCAACAGGAGGACTTATGACCTACC 587

648 CG 649
    ||
588 CG 589
```

M. Tuberculosis* x *M. Avium

Percent Similarity: 77.504 Percent Identity: 77.504

```
             .         .         .         .         .
  1 TCATAGCAGGCCTCCTCTTGGGTCCACAACGCCCGCATCGCCTCGAGGTA 50
    || |||| ||| ||||| | |||||||| |||||||||||| || |||||
  1 TCGTAGCTGGCTTCCTCGTCGGTCCACAGCGCCCGCATCGCTTCCAGGTA 50
             .         .         .         .         .
 51 TTCGCGCAGCATGGTGCGGCGGCGTCCGGGTGGCACACCATGATCGACGA 100
    ||||||||||||||||||||| || || |  ||||| || || ||| |||
 51 TTCGCGCAGCATGGTGCGGCGCCGGCCCGCCGGCACGCCGTGGTCGGCGA 100
```

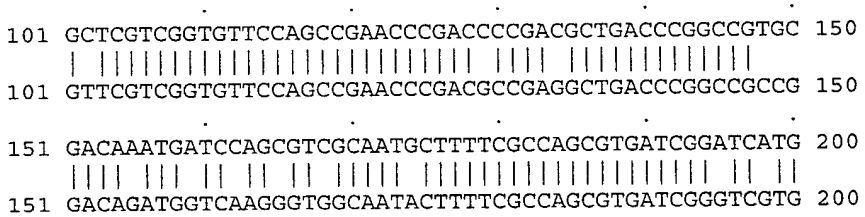
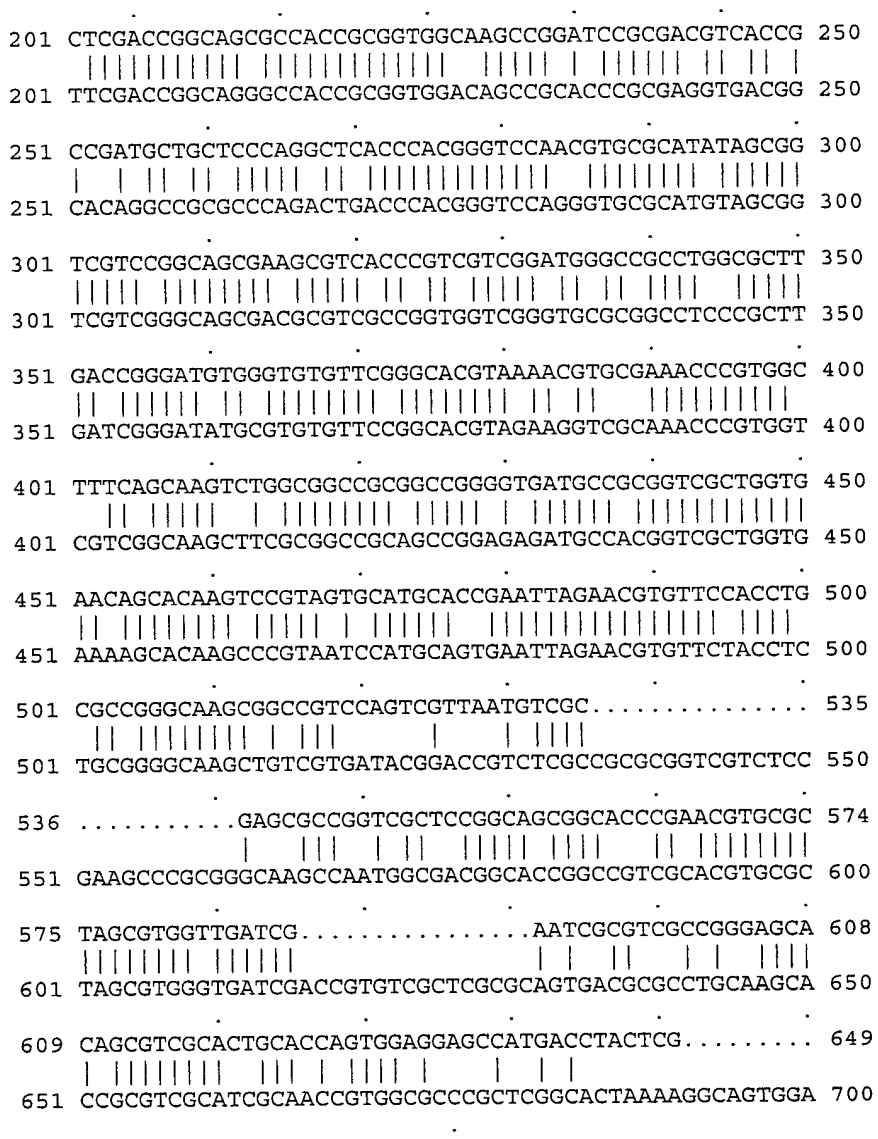


Figure 10-continued



***M. Tuberculosis* x *M.* Intracellulare**

Percent Similarity: 43.220 Percent Identity: 43.220

```
             .         .         .         .         .
 51 TTCGCGCAGCATGGTGCGGCGGCGTCCGGGTGGCACACCATGATCGACGA 100
                                 |  |  | ||  |   |
  1 ................................GTTCTACCTGTGCTGAGC 18

             .         .         .         .         .
101 GCTCGTCGGTGTTCCAGCCGAACCCGACCCCGACGCTGACCCGGCCGTGC 150
      | ||||| | | | |   | || |   |   |      ||||  ||
 19 AAGCTCCGGTGATACCGACCGTCTCGCCGGAGGGCCGCCGGGGGCCTCGC 68

             .         .         .         .         .
151 GACAAATGATCCAGCGTCGCAATGCTTTTCGCCAGCGTGATCGGATCATG 200
     |  | ||     |         | ||| |   ||||  |   | | ||
 69 CGCCCAAGACAGTGGCGGCGCCACCGGTTCCCGCACGTGCGC.TAGCGTG 117
```

Figure 10-continued

```
             .         .         .         .         .
201 CTCGACCGGCAGCGCCACCGCGGTGGCAAGCCGGATCCGCGACGTCACCG 250
      || || | |||    |||  ||    | ||  | || |   || ||
118 GGTGATCGACCGCG...TCGCAATGCGGTGACGCGCCTGCAAGCACAGCG 164

             .         .         .         .         .
251 CCGATGCTGCTCCCAGGCTCACCCACGGTCCAACGTGCGCATATAGCGG 300
     ||  |  | ||  ||| | | | |||  |  |   || |   ||||
165 TCGCATCGCCACCGCGGCGCCCGCTCGGCACTTAAAGGCACTGGTAGCAA 214

             .         .         .         .         .
301 TCGTCCGGCAGCGAAGCGTCACCCGTCGTCGGATGGGCCGCCTGGCGCTT 350
      |   |       | | | |
215 CAGGAGGAGCCATGACCTACTC........................... 236
```

M. Tuberculosis* x *M. Simiae

Percent Similarity: 75.655 Percent Identity: 75.655

```
             .         .         .         .         .
  1 TCATAGCAGGCCTCCTCTTGGGTCCACAACGCCCGCATCGCCTCGAGGTA 50
    || ||   ||| || || || ||||||| ||||||||| || || |||||
  1 TCGTATTGGGCTTCTTCCTGCGTCCACAGCGCCCGCATGGCTTCCAGGTA 50

             .         .         .         .         .
 51 TTCGCGCAGCATGGTGCGGCGGCGTCCGGGTGGCACACCATGATCGACGA 100
     ||||||||||||| || |||||  | || |||||     || ||| | |
 51 CTCGCGCAGCATGGTCCGCCGGCGCGCCGGCGGCACGTTGTGGTCGGCCA 100

             .         .         .         .         .
101 GCTCGTCGGTGTTCCAGCCGAACCCGACCCCGACGCTGACCCGGCCGTGC 150
    | |||||||||||||| |||||||||| || || |||||||| |||
101 GTTCGTCGGTGTTCCAACCGAACCCGACGCCCACACTGACCCGTCCGCCG 150

             .         .         .         .         .
151 GACAAATGATCCAGCGTCGCAATGCTTTTCGCCAGCGTGATCGGATCATG 200
    |||| ||| ||||| || || ||||||||||||||||||||||| || ||
151 GACAGATGGTCCAGGGTGGCGATGCTTTTCGCCAGCGTGATCGGGTCGTG 200

             .         .         .         .         .
201 CTCGACCGGCAGCGCCACCGCGGTGGCAAGCCGGATCCGCGACGTCACCG 250
    |||||| |||||||| ||||||||||   || || | |||||| || ||||
201 CTCGACGGGCAGCGCGACCGCGGTGGACAGTCGCACCCGCGAGGTGACCG 250

             .         .         .         .         .
251 CCGATGCTGCTCCCAGGCTCACCCACGGTCCAACGTGCGCATATAGCGG 300
```

```
    |  | || || ||||| || ||||||||||||| ||||||||| ||||||
251 CGCACGCCGCGCCCAGACTGACCCACGGGTCCAGCGTGCGCATGTAGCGG 300
             .         .         .         .         .
301 TCGTCCGGCAGCGAAGCGTCACCCGTCGTCGGATGGGCCGCCTGGCGCTT 350
    ||||| ||||||||  |||| |||||||| ||||||||||||| ||||||
301 TCGTCGGGCAGCGATTCGTCGCCCGTCGTGGGATGGGCCGCCTCGCGCTT 350
             .         .         .         .         .
351 GACCGGGATGTGGGTGTGTTCGGGCACGTAAAACGTGCGAAACCCGTGGC 400
    || ||||||||| |||||||| |||||||| |||||    || || |||
351 GATCGGGATGTGAGTGTGTTCTGGCACGTAGAACGTTGTGAAGCCATGGT 400
             .         .         .         .         .
401 TTTCAGCAAGTCTGGCGGCCGCGGCCGGGGTGATGCCGCGGTCGCTGGTG 450
      || || ||| |||| || || ||||||| |||||| || || ||||||
401 CGTCGGCGAGTTTGGCCGCGGCCGCCGGGGCGATGCCCCGATCACTGGTG 450
             .         .         .         .         .
451 AACAGCACAAGTCCGTAGTGCATGCACCGAATTAGAACGTGTTCCACCTG 500
    || ||||| || ||||| | ||||||| |||||||||||||||| ||||
451 AAAAGCACGAGCCCGTAATCCATGCACAGAATTAGAACGTGTTCTACCTC 500
```

Figure 10-continued

```
             .         .         .         .         .
501 CGCCGGGCAAGCGGCCGTCCAGTCGTTAATGTCGCGA............. 537
     |  | ||||||||||  |    |||  |      ||
501 TGTGGAGCAAGCGGCCCCCGCTACGTCGACCCGCAGACGGCCGCTGAGA 550

             .         .         .         .         .
538 .......................GCGCCGGTCGCTCCGGCAGCGGCACCC 564
                           | |||||||||||| ||     | | |
551 CGATCGCTCCTGGTCGCGCCTAGGGGCCGGTCGCTCCCGCGCACCCGCTC 600
             .         .         .         .         .
565 GAACGTGCGCTAGCGTGGTTGATCGAATCGCGTCGCCGGGAGCACAGCGT 614
    |||||||||||||||||||||||||           ||  | | | |
601 GAACGTGCGCTAGCGTGGTTGATCGGTCGCGCGTAACGCAAACGCGGGCA 650
             .         .         .         .         .
615 CGCACTG....CACCAGTGGAGGAGCCATGACCTACTCG........... 649
    ||| |||    ||||   ||  ||||| ||        |
651 CGCCCTGGCGTCACCGACGGGCGAGCCCTGCAGACACGGCGTCGCACTGC 700
```

Figure 11A. Organisation of the rrn operon of Pseudomonas aeruginosa (Ps. Ae), Burkholdenia cepacia (Bu. ce) and Stenotrophomonas maltophilia (St. ma).

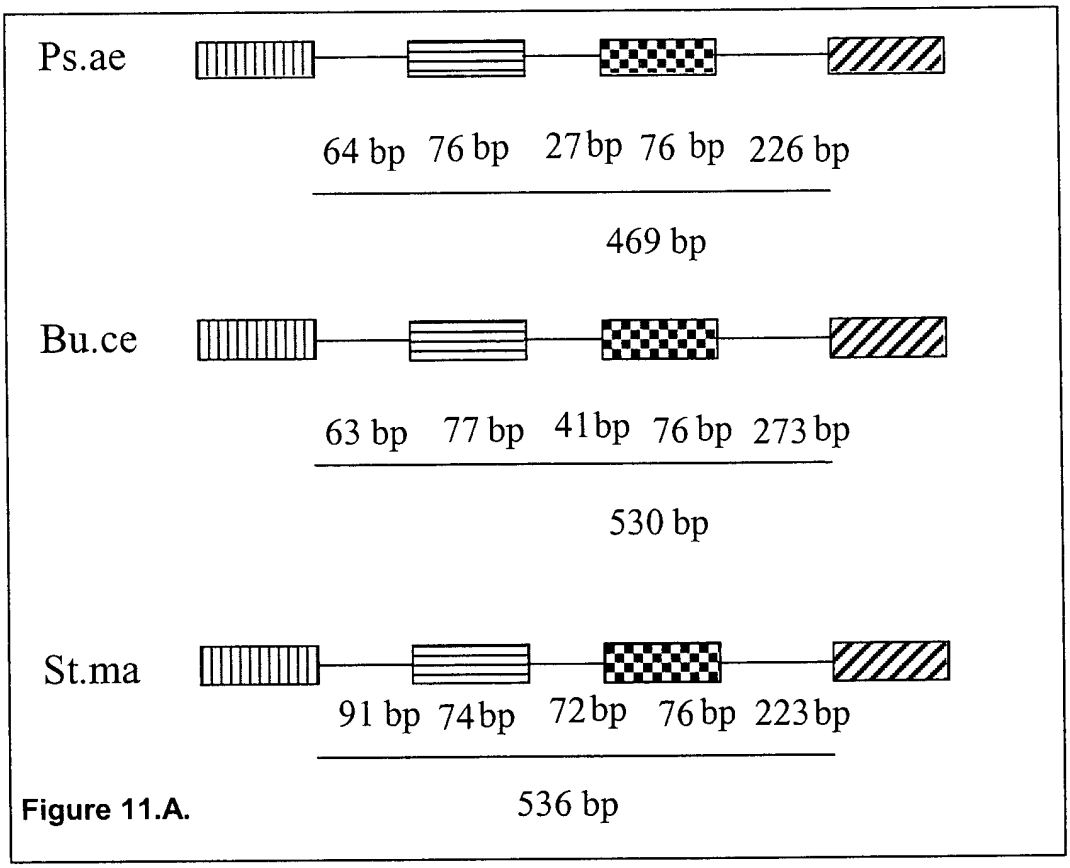


Figure 11.A.

= RNA 16S (3 ' end)

= tRNA Isoleucine

= tRNA Alanine

= tRNA 23S (5 ' end)

Figure 11B. Comparison of the sequences flanking the regions encoding 16S and 23S RNA from Pseudomonas aeruginosa (Ps. Ae) (SEQ ID NO 76), Burkholdenia cepacia (Bu. ce) (SEQ ID NO 77). CNS (consensus).

```
         1                                                        60
Bu.ce.   ---------- ---------- -----tta-- ------g--- ---------- -----a----
Ps.ae.   ---------- ---------- -----gct-- ------a--- ---------- -----g----
   CNS   GCCCGTCACA CCATGGGAGT GGGTT---CC AGAAGT-GCT AGTCTAACCG CAAGG-GGAC

         61                                                      120
Bu.ce.   ---c------ -tag------ ---------- ---------- ---------- ---tc----g
Ps.ae.   ---t------ -agt------ ---------- ---------- ---------- ---gg----c   16S
   CNS   GGT-ACCACG G---GATTCA TGACTGGGGT GAAGTCGTAA CAAGGTAGCC GTA--GGAA-

         121                                                     180
Bu.ce.   g--------- ---------- -tcca--gct ----.--.a- aagt-g---g -t---g-tt-
Ps.ae.   c--------- ---------- -aatc--aga ----a--tt- ttca-a---t -c---a-ga-
   CNS   -TGCGGCTGG ATCACCTCCT T----GA--- TCTC-GC--C ----T-AGC- C-CAC-C--A

         181                                                     240
Bu.ce.   -cg---gt-a attaaa-ac- ---tcag--- ---------- ---c------ ---a-cgt-t
Ps.ae.   -.t---tg-t tcactg-tt- ---gatt--- ---------- ---t------ ---g-acc-c
   CNS   T--GCT--A- ------G--A GAC----GGG TCTGTAGCTC AGT-GGTTAG AGC-C---C-   tRNA

Ile
         241                                                     300
Bu.ce.   --------cg -g-----ttg ---------c aa-------- ----t-gtc- -gc---aaca
Ps.ae.   --------.t -a-----gca ---------t gc-------- ----a-...- -tt---gtgc
   CNS   TGATAAGG-- G-GGTCG--- GTTCGAATC- --CCAGACCC ACCA-T---T G--GGT----

         301                                                     360
Bu.ce.   ca-c---gg- a-atctg--- atg---g--- ---------- -------a-- ---------a   tRNA-
Ps.ae.   tg-g---tc- g-.....--- ...---c--- ---------- -------g-- ---------c
   CNS   --C-TGA--C -A-----TAC ---GGG-CAT AGCTCAGCTG GGAGAGC-CC TGCTTTGCA-   ala

         361                                                     420
Bu.ce.   -----.---- gtcg------ ---cgtc--c -------a-- -acc---gct --gggc-t-g
Ps.ae.   -----a---- agga------ ---tcct--g -------.-- -taa---... --.....-c-t
   CNS   GCAGG-GGTC ----GTTCGA TCC----TG- CTCCACC-AT C---AAC--- AA----T-G-

         421                                                     480
Bu.ce.   ttc-ga-a-t ---cc--gaa --ttgc-t-- gcg-----gc cag--a-agg a-at--a---
Ps.ae.   cga-ag-t-a ---at--atg --cgtg-a-- aac------. .tt--t-gtc t-tg--c---
   CNS   ---A--C-C- GAA--GA--- TT----A-TG ---ATTGA-- ---TC-G--- -T--CA-CAG

         481                                                     540
Bu.ce.   -tatcgg--g tc-------- -c---ct--a agaa---a-- aatttg---- gcg----cgt
Ps.ae.   -.....a--. ..-------- -a---tc--. ....---t-- ......---- ..------..
   CNS   A------CT- --GTTCTTTA A-AAT--GG- ----GTA-GT ------GATA ---GAAG---

         541                                                     600
Bu.ce.   ct-g---tg- -cg--ga-a- -a-ccggg-t -----tg-a- -g-tgt-tct c--g--ga-t
Ps.ae.   ..-a---ct- -.a--..-t- -c-ttcac-g -----ca-.- -a-gtc-agg t--a--.t-g
   CNS   --T-AGA--G A--TG--A-C T-T-----T- GTGAT--T-T C-A---A--- -AA-AT--T-

         601                                                     660
Bu.ce.   ---ac--t-- -ttt-actc- ---ggaa-a- ---ac--c-c ga-aac---a cc-g----g-
Ps.ae.   ---gt--.-- -cgc-....- ---....-t- ---.g--t-. tc-tct---c ag-a----c-
   CNS   CGA--TC-AA G---G----A ATT----T-C GGC--AA-G- --G---TCA- --T-TAAC-A

         661                                                     720
Bu.ce.   --ca-ac-.. c------g-- -----c---c ---t----gt ---------- ----------
Ps.ae.   --tt-ct-gg g------t-- -----t---g ---c----ac ---------- ----------   23S
   CNS   GA--G--T-- -GTTATA-GG TCAAG-GAA- AAG-GCAT-- GGTGGATGCC TTGGCRRTCA
```

Figure 12. Discrimination by multiplex PCR.

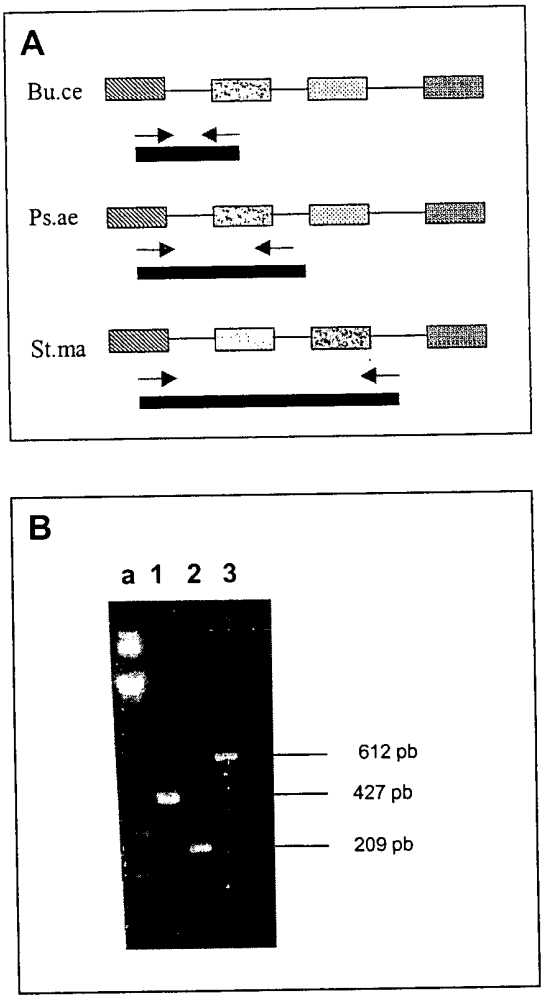


Figure 13. Multiplex PCR sensibility validation

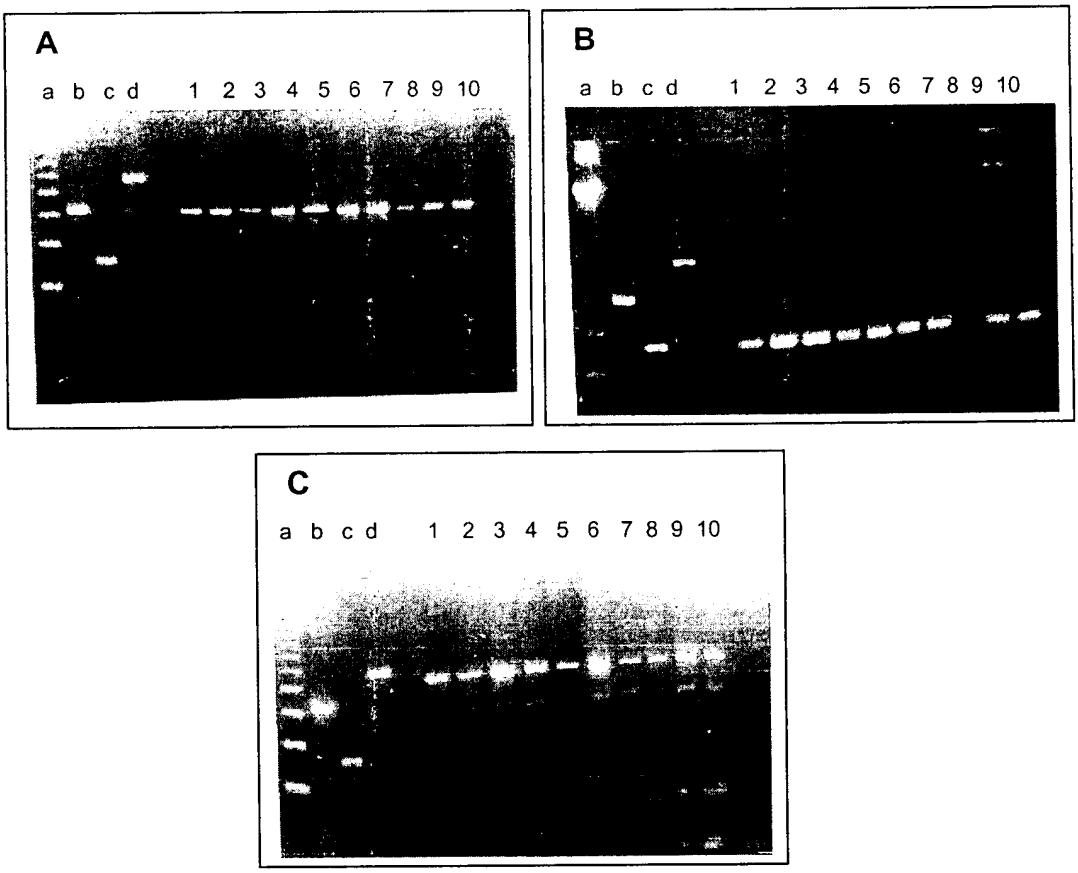


Figure 14. Multiplex PCR specificity validation

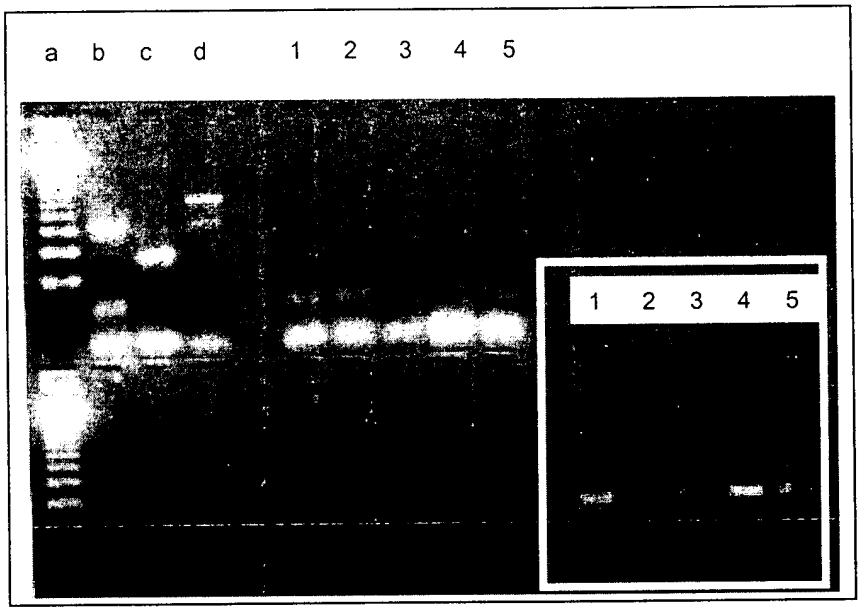


Figure 15. Reverse hybrisitaion for the discrimination between *Ps. aeruginosa*, *Bu. cepacia* and *St. maltophilia*

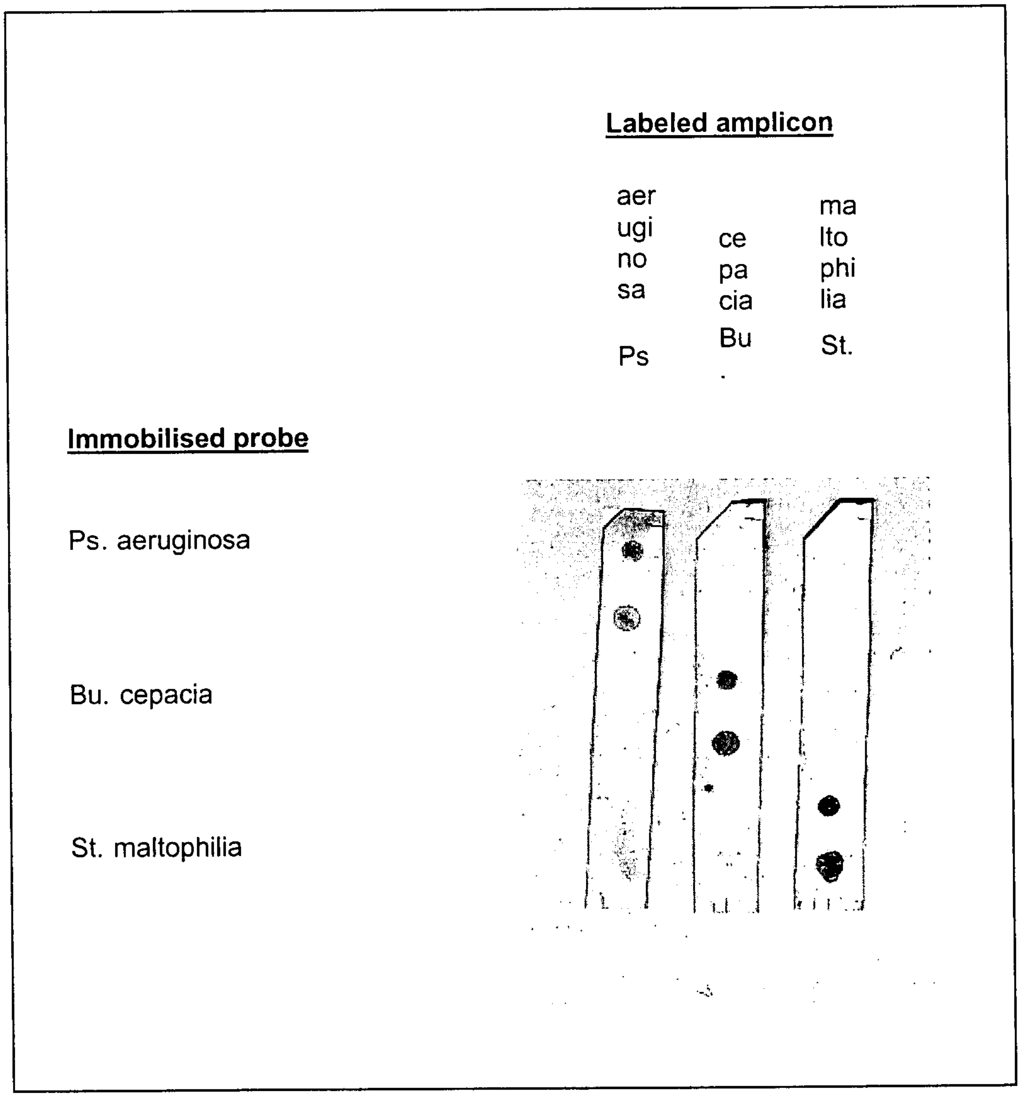


Figure 16. Visualization of the second *rrn* operon from *Ps. putida*

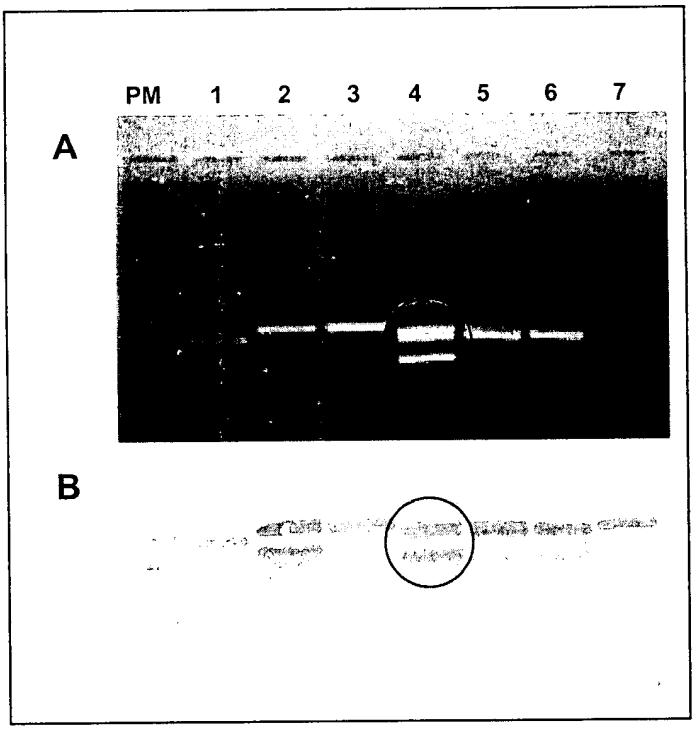


Figure 17. Alignment of the two *rrn* operon sequences from *Ps. putida.* First (top) sequence is SEQ ID NO 78, second (bottom) sequence is SEQ ID NO 79.

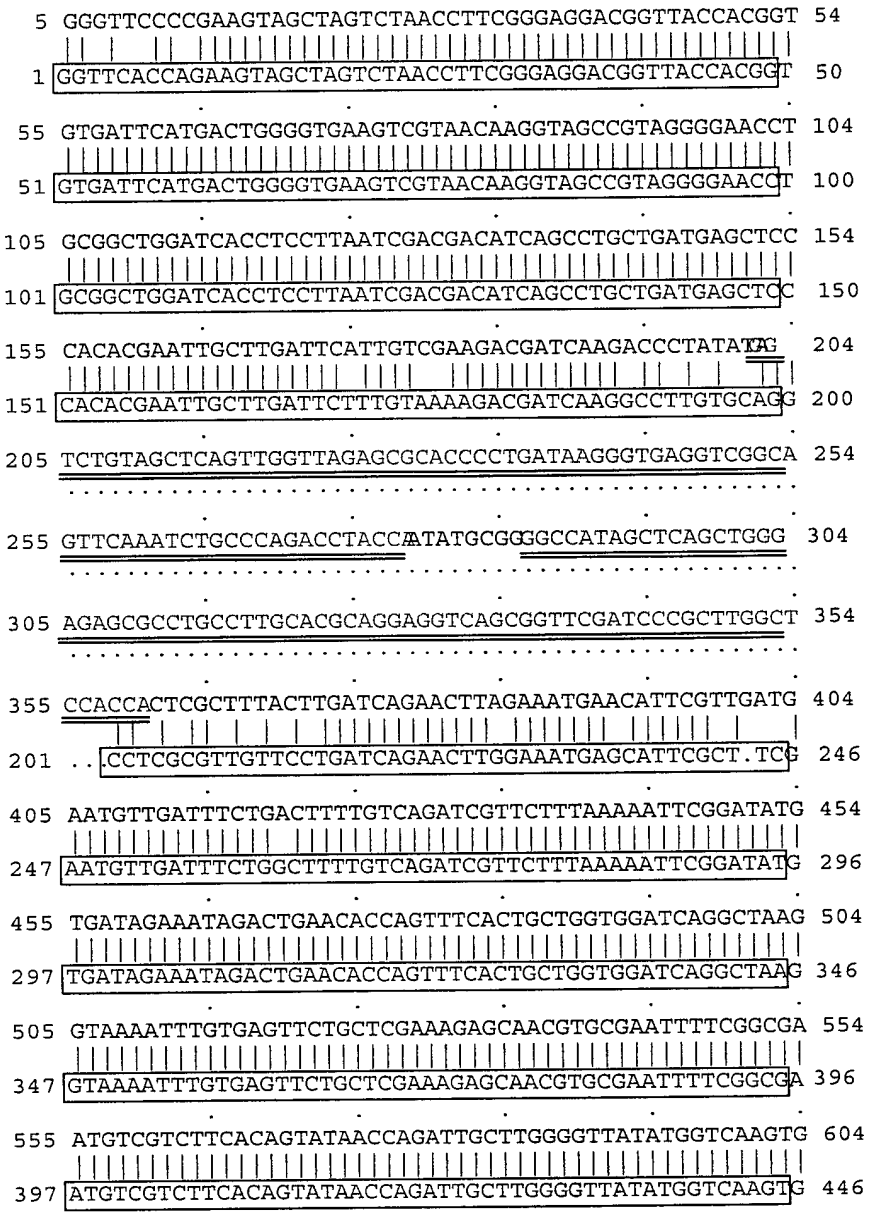


Figure 18. Alignment and consensus sequence between *Pseudomonas aeruginosa* (ps.msf{padfc}), *Burkholderia cepacia* (ps.msf{pcdfg} and *Stenotrophomonas maltophilia* (ps.msf{xmdfa}).

```
                    1                                                  60
ps.msf{padfc}  ---------- ---------- gg---gct-- -----ta-c- --tc-----g caa--g--a-
ps.msf{pcdfg}  ---------- ---------- gg---tta-- -----tg-c- --tc-----g caa--a--a-
ps.msf{xmdfa}  ---------- ---------- tt---gca-- -----ca-g- --ct-----t tcg--a--g-
    Consensus  GCCCGTCACA CCATGGGAGT --GTT---CC AGAAG--G-T AG--TAACC- ---GG-GG-C

                   61                                                 120
ps.msf{padfc}  -g-tac---- -agtgattc- ---------- ---------- ---------- ---gg----c
ps.msf{pcdfg}  -g-cac---- -taggattc- ---------- ---------- ---------- ---tc----g
ps.msf{xmdfa}  -c-t.g---- -t.gctgcg- ---------- ---------- ---------- ---tc----g
    Consensus  G-T---CACG G--------A TGACTGGGGT GAAGTCGTAA CAAGGTAGCC GTA--GGAA-

                  121                                                 180
ps.msf{padfc}  c--------- ---------- -aatc-..-a gatct-ag-t t-ttcataa- -tccca-a-g
ps.msf{pcdfg}  g--------- ---------- -tcca-..-g cttct-.g-. a-aagttga- -gctca-g-t
ps.msf{xmdfa}  g--------- ---------- -ttga-ca-a gacag-at-g t-ctgtcgg- -gtctt-a-a
    Consensus  -TGCGGCTGG ATCACCTCCT T----G--A- -----C--C- -C-------G C-----C-C-

                  181                                                 240
ps.msf{padfc}  a-t.tg--tg -ttcactggt t..ag--gat tg--t-tg-a gctc---tgg --aga-cg-a
ps.msf{pcdfg}  t-tcgg--gt -aattaaaga c..ag--tca gg--t-tg-a gctc---cgg --aga-ca-c
ps.msf{xmdfa}  a-gtac--gc -ttcagagaa tcaca--ggc ca--c-ga-g tgag---ccc --ttg-gc-t
    Consensus  -A----CT-- A--------- -----AC--- --GG-C--T- ----AGT--- TT---G--C-

                  241                                                 300
ps.msf{padfc}  cccc-g-taa --.t-a-gt- ggcag--cg- -t-tgcccag ac-caccaat ...t-ttg-t
ps.msf{pcdfg}  gtct-g-taa --cg-g-gt- gttgg--cg- -t-caaccag ac-caccatt gtct-gcg-t
ps.msf{xmdfa}  tagc-c-gct --ga-a-ca- ctgct--gc- -g-aggggtc gt-ggttcga tccc-aca-.
    Consensus  ----T-A--- GG--G-G--C -----TT--A A-C------- --C------- ----G---G-

                  301                                                 360
ps.msf{padfc}  gtgctg-g-- atccga.... .---...g-g c-a-ag-tc- -ct-gga-ag -gc-tgct-t
ps.msf{pcdfg}  aacaca-c-- aggcaaatct g---atgg-g g-a-ag-tc- -ct-gga-ag -ac-tgct-t
ps.msf{xmdfa}  ctccac-a-- ttcgagctgt a---cgaa-t c-c-tt-ga- -.a-ccc-ca -at-catg-g
    Consensus  ------C-TG ---------- -TAC----G- -C-T--C--A G--G---G-- C--C----T-

                  361                                                 420
ps.msf{padfc}  gc-cgcagga ggtcaggag- ---atc-tcc t-gg---cac c.a-ctaaaa -...aa....
ps.msf{pcdfg}  gc-agcagg. ggtcgtcgg- ---atc-cgt c-gc---cac caa-caccaa -gctaagggc
ps.msf{xmdfa}  ct-ctttttg aaaaagcct- ---ggt-tg. .-ag---agg tgg-tagacg -accctgata
    Consensus  --A------- ---------T TCG---C--- -T--CTC--- ---T------ C---------

                  421                                                 480
ps.msf{padfc}  tc-tcgaaag -tcagaaat- -atg-.tcgt g-atgaac-- -ga...tttc t-gtctttg-
ps.msf{pcdfg}  tt-gttcaga -actgaacc- -gaa-.tttg c-ttggcg-- -gagccagtc a-aggatat-
ps.msf{xmdfa}  ag-gtgaggt -ggtagttc- -gtc-accca g-cccacc-- -..ctctgaa t-acgcata-
    Consensus  --G------- C--------G A---T----- -A------AT T--------- -G-------C

                  481                                                 540
ps.msf{padfc}  -cca--.... .ac-...gtt -t-t-aa-a- tc--.....g tat--.... .g-t-...-a
ps.msf{pcdfg}  -aca--tatc ggc-gtcgtt -t-t-ac-a- ct--aagaag taa--aattt gg-t-gcg-a
ps.msf{xmdfa}  -ttc--tct. ...-tatacg -a-c-gc-c- gt--ctggta cgt--tcttt ta-a-ctt-t
    Consensus  A---GA---- ---T------ C-T-A--A-T --GG------ ---GT----- --A-A---G-
```

Figure 18 -continued

```
                 541                                                        600
ps.msf{padfc}    ag.....ta- -actga.atg ..at--c-tt cactg--ga- cat.tca-gt caaggt-aa.
ps.msf{pcdfg}    agcgtcttg- -atggacgtg gaaa--a-cc gggtt--ga- tgtatcg-tg tatctc-ag.
ps.msf{xmdfa}    gacgtagcg- -cgtttgaga tgtt--a-ca gacgt--cg- gaggcta-gg cgagag-cgc
    Consensus    ---------A G--------- ----CT-T-- -----GT--T -------A-- ------A---

                 601                                                        660
ps.msf{padfc}    -t.ttg-.ga gt-c.aa-cg cg....a--- ....-t-.-- -.gaatg.tc gtcttcacag
ps.msf{pcdfg}    -tgatt-.ga ac-ctaa-tt tgactca--- ggaa-a-.-- -acaacgcga gaactcaacc
ps.msf{xmdfa}    -agtct-ttt at-gatt-ag tcgttat--- cgta-c-g-- -tttgtaccc ccgggtcgtg
    Consensus    A-----C--- --T----G-- -------ATT ----T-C-GG C--------- ----------

                 661                                                        720
ps.msf{padfc}    -a----c..- -attgct-gg g------t-- -----t---g ---c---tac ----------
ps.msf{pcdfg}    -g----g..- -acagac-.. c------g-- -----c---c ---t---tgt ----------
ps.msf{xmdfa}    -g----cca- -gcaact-gc g------t-- -----c---t ---c---cac ----------
    Consensus    T-TAAC---A G------T-- -GTTATA-GG TCAAG-GAA- AAG-GCA--- GGTGGATGCC

                 721            737
ps.msf{padfc}    ---------- -------
ps.msf{pcdfg}    ---------- -------
ps.msf{xmdfa}    ---------- -------
    Consensus    TTGGCRRTCA SAGGCGA
```

Figure 19. Alignement between *Pseudomonas aeruginosa* (ps.msf{padfc}) (SEQ ID NO 80), *Burkholderia cepacia* (ps.msf{pcdfg} (SEQ ID NO 81) and *Stenotrophomonas maltophilia* (ps.msf{xmdfa}) (SEQ ID NO 82), as in Figure 18 but without consensus sequence.

```
Symbol comparison table: GenRunData:pileupdna.cmp  CompCheck: 6876

             GapWeight: 1
       GapLengthWeight: 1

 ps.msf  MSF: 737  Type: N
Name: padfc           Len:   737  Check: 1233  Weight:  1.00
Name: pcdfg           Len:   737  Check:  773  Weight:  1.00
Name: xmdfa           Len:   737  Check: 3019  Weight:  1.00

//

       1                                                    50
padfc  GCCCGTCACA CCATGGGAGT GGGTTGCTCC AGAAGTAGCT AGTCTAACCG
pcdfg  GCCCGTCACA CCATGGGAGT GGGTTTTACC AGAAGTGGCT AGTCTAACCG
xmdfa  GCCCGTCACA CCATGGGAGT TTGTTGCACC AGAAGCAGGT AGCTTAACCT

       51                                                   100
padfc  CAAGGGGGAC GGTTACCACG GAGTGATTCA TGACTGGGGT GAAGTCGTAA
pcdfg  CAAGGAGGAC GGTCACCACG GTAGGATTCA TGACTGGGGT GAAGTCGTAA
xmdfa  TCGGGAGGGC GCTT.GCACG GT.GCTGCGA TGACTGGGGT GAAGTCGTAA

       101                                                  150
padfc  CAAGGTAGCC GTAGGGGAAC CTGCGGCTGG ATCACCTCCT TAATCG..AA
pcdfg  CAAGGTAGCC GTATCGGAAG GTGCGGCTGG ATCACCTCCT TTCCAG..AG
xmdfa  CAAGGTAGCC GTATCGGAAG GTGCGGCTGG ATCACCTCCT TTTGAGCAAA

       151                                                  200
padfc  GATCTCAGCT TCTTCATAAG CTCCCACACG AAT.TGCTTG ATTCACTGGT
pcdfg  CTTCTC.GC. ACAAGTTGAG CGCTCACGCT TATCGGCTGT AAATTAAAGA
xmdfa  GACAGCATCG TCCTGTCGGG CGTCTTCACA AAGTACCTGC ATTCAGAGAA

       201                                                  250
padfc  T..AGACGAT TGGGTCTGTA GCTCAGTTGG TTAGAGCGCA CCCCTGATAA
pcdfg  C..AGACTCA GGGGTCTGTA GCTCAGTCGG TTAGAGCACC GTCTTGATAA
xmdfa  TCACAACGGC CAGGCCGATG TGAGAGTCCC TTTTGGGCCT TAGCTCAGCT

       251                                                  300
padfc  GG.TGAGGTC GGCAGTTCGA ATCTGCCCAG ACCCACCAAT ...TGTTGGT
pcdfg  GGCGGGGGTC GTTGGTTCGA ATCCAACCAG ACCCACCATT GTCTGGCGGT
xmdfa  GGGAGAGCAC CTGCTTTGCA AGCAGGGGTC GTCGGTTCGA TCCCGACAG.

       301                                                  350
padfc  GTGCTGCGTG ATCCGA.... .TAC...GGG CCATAGCTCA GCTGGGAGAG
pcdfg  AACACACCTG AGGCAAATCT GTACATGGGG GCATAGCTCA GCTGGGAGAG
xmdfa  CTCCACCATG TTCGAGCTGT ATACCGAAGT CCCTTTCGAA G.AGCCCGCA

       351                                                  400
padfc  CGCCTGCTTT GCACGCAGGA GGTCAGGAGT TCGATCCTCC TTGGCTCCAC
pcdfg  CACCTGCTTT GCAAGCAGG. GGTCGTCGGT TCGATCCCGT CTGCCTCCAC
xmdfa  CATCCATGTG CTACTTTTTG AAAAAGCCTT TCGGGTCTG. .TAGCTCAGG
```

```
       401                                                  450
padfc  C.ATCTAAAA C...AA.... TCGTCGAAAG CTCAGAAATG AATGT.TCGT
pcdfg  CAATCACCAA CGCTAAGGGC TTGGTTCAGA CACTGAACCG AGAAT.TTTG
xmdfa  TGGTTAGACG CACCCTGATA AGGGTGAGGT CGGTAGTTCG AGTCTACCCA

       451                                                  500
padfc  GAATGAACAT TGA...TTTC TGGTCTTTGC ACCAGA.... .ACT...GTT
pcdfg  CATTGGCGAT TGAGCCAGTC AGAGGATATC AACAGATATC GGCTGTCGTT
xmdfa  GACCCACCAT T..CTCTGAA TGACGCATAC ATTCGATCT. ...TTATACG

       501                                                  550
padfc  CTTTAAAAAT TCGG.....G TATGT..... .GATA...GA AG.....TAA
pcdfg  CTTTAACAAT CTGGAAGAAG TAAGTAATTT GGATAGCGGA AGCGTCTTGA
xmdfa  CATCAGCACT GTGGCTGGTA CGTGTTCTTT TAAAACTTGT GACGTAGCGA

       551                                                  600
padfc  GACTGA.ATG ..ATCTCTTT CACTGGTGAT CAT.TCAAGT CAAGGTAAA.
pcdfg  GATGGACGTG GAAACTATCC GGGTTGTGAT TGTATCGATG TATCTCAAG.
xmdfa  GCGTTTGAGA TGTTCTATCA GACGTGTCGT GAGGCTAAGG CGAGAGACGC

       601                                                  650
padfc  AT.TTGC.GA GTTC.AAGCG CG....AATT ....TTC.GG C.GAATG.TC
pcdfg  ATGATTC.GA ACTCTAAGTT TGACTCAATT GGAATAC.GG CACAACGCGA
xmdfa  AAGTCTCTTT ATTGATTGAG TCGTTATATT CGTATCCGGG CTTTGTACCC

       651                                                  700
padfc  GTCTTCACAG TATAACC..A GATTGCTTGG GGTTATATGG TCAAGTGAAG
pcdfg  GAACTCAACC TGTAACG..A GACAGACT.. CGTTATAGGG TCAAGCGAAC
xmdfa  CCGGGTCGTG TGTAACCCAA GGCAACTTGC GGTTATATGG TCAAGCGAAT

       701                                     737
padfc  AAGCGCATAC GGTGGATGCC TTGGCRRTCA SAGGCGA
pcdfg  AAGTGCATGT GGTGGATGCC TTGGCRRTCA SAGGCGA
xmdfa  AAGCGCACAC GGTGGATGCC TTGGCRRTCA SAGGCGA
```